

REMARKS

Claims 12, 14-20 and 31-34 are amended. Claim 35 is added. Claims 22-30 have been withdrawn from consideration by the Examiner. Claims 12-14, 16-21 and 31-35 are active and under consideration.

At the outset, Applicants wish to thank Examiner Marvich for the helpful and courteous discussion conducted with their U.S. representative, on March 17, 2009. The supporting remarks for patentability are consistent with the remarks made during the discussion with the Examiner.

Claims 12-15, 19-21 and 31-34 stand rejected under 35 USC 102(b) as being anticipated by *Poquet et al*, J. Bacteriology, 1998, Vol. 180, pages 1904-1912.

However, this reference fails to disclose or suggest the claimed invention.

Notably, *Poquet et al* (J. Bacteriology, 1998, Vol. 180: 1904-1912) disclose a plasmid pFUN comprising sequence accession number GenBank U95834 which contains the sequence named nlp3 (see attached copy of NCBI description of GenBank U95834). The sequence accession number U95834 consists of:

- i) p_{Zn} promoter;
- ii) a sequence encoding ZitR; and
- iii) part of sequence coding for ZitS.

This sequence has been cloned in the polylinker of pFUN as to obtain expression of a fusion peptide n1p3/ Δ Nuc. Therefore, *Poquet et al* disclose a plasmid containing the p_{Zn} promoter (promoter sequence corresponding to SEQ ID NO: 1 of claimed expression cassette), a sequence encoding ZitR, the N-terminal part of ZitS fused with the sequence coding for Δ Nuc, followed by the downstream restriction sites of the polylinker.

Amended claims 12 and 15 clearly relate to an expression cassette which does not contain

a sequence encoding any part of *L. lactis* ZitS. Consequently, the amended claims are clearly not anticipated by *Poquet et al.*

It is also clear that *Poquet et al* would have failed to have rendered the claimed invention obvious at the time it was made. *Poquet et al* identified among others a sequence (U95834 GenBank sequence) which contains n1p3 coding sequence. *Poquet et al* are only interested in exported peptide n1p3, and are totally silent about a possible function of the other nucleotide sequences contained in U95834 GenBank sequence. Nothing in the disclosure of *Poquet et al* or in accession number U95834 report would have suggested to the artisan that any other sequences contained in U95834 sequence could have a regulating function or code for a protein. See the attached NCBI description of GenBank U95834.

Therefore the person skilled in the art would not have been motivated to isolate specifically the nucleotide sequence corresponding to p_{zn} promoter and sequence encoding ZitR from sequence GenBank accession number U95834 in order to engineer an expression cassette which has the characteristic to regulate expression of a gene according to the concentration of zinc in the culture medium.

Further, *Poquet et al* would not have enabled one skilled in the art to do so in any event.

Hence, this ground of rejection is unsustainable and should be withdrawn.

Claims 12-21 and 31-34 stand rejected under 35 USC 112, first paragraph, as the present specification ostensibly does not provide enablement for any embodiment of expression cassettes other than that containing SEQ ID NO: 1 operably linked to nucleotides 357-794 of SEQ ID NO: 2 further operably linked to a restriction site.

However, it is believed that the present claims are fully enabled by the present specification for the following reasons. The comments set forth below refer to Annex 1 and Annex 2, copies of

which are attached to this response.

First, the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

Second, Annex 1 shows the results of a BLAST search performed against the nr database which includes all the known protein sequences of all living organisms. Among these sequences, the only ones which share at least 80% identity with ZitR of *L. lactis* subsp. *Lactis* II1403 (GenBank AAK06214) are ZitR proteins, namely the ZitR protein of *L. lactis* subsp. *cremoris* MG1363 (88% identity) and the ZitR protein of *L. lactis* subsp. *cremoris* SK11 (89% identity). As a matter of fact there is no protein having at least 80% identity with GenBank AAK06214 which is not a ZitR protein. The next proteins which have the higher homology with ZitR are Streptococcus proteins which have at most 54% identity with GenBank AAK06214. Therefore, it is very unlikely that one can isolate a protein having 80% identity or more with GenBank AAK06214 which is not a ZitR protein.

Annex 2 shows the results of a BLAST search performed against the whole genome sequences of *L. lactis* subsp. *Lactis* II1403, *L. lactis* subsp. *cremoris* MG1363 and *L. lactis* subsp. *cremoris* SK11. There is no lactococcal protein, other than the ZitR proteins, having more than 38% identity with GenBank AAK06214.

Therefore using a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9 of the instant application for screening a lactococcal DNA library, one of skill in the art would be able to easily discriminate a sequence encoding a ZitR protein from other lactococcal sequences.

Moreover, only the whole genome sequence of *L. lactis* subsp. *Lactis* II1403 (which was published in 2001) was available before the invention was made. The genome sequences of *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363 were only available in GenBank in 2006 and 2007 respectively. It is pointed out, however, that besides indicating GenBank AAK06214 as the reference sequence for a ZitR protein, the present application discloses another sequence encoding a ZitR protein, namely nucleotides 357 to 794 of SEQ ID NO:9, which encodes the ZitR protein of *lactis* subsp. *cremoris* MG1363.

Actually, the knowledge of the lactococcal genome sequences is not necessary to practice the claimed invention. As indicated above, one of ordinary skill in the art could have easily obtained polynucleotides encoding lactococcal ZitR proteins by screening a DNA library of a *Lactococcus* with a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9.

BLAST results are provided herewith solely to evidence that the lactococcal genome does not contain any protein having more than 80% identity with GenBank AAK06214 which is not a ZitR protein.

Second, the two BLAST searches and results thereof noted above indicate that the present specification does in fact satisfy both the statutory enablement requirement under 35 USC 112, first paragraph, and the case law tests therefor cited by the Examiner.

Specifically, under the case law tests for enablement articulated in In re Wright and In re Fisher, cited by the Examiner, it is clear that since nucleotide sequences having more than 80% identity with GENBANK AAK06214 could easily be obtained by routine screening with a probe (as described above), undue experimentation would not be required.

Claims 12-16, 18-20 and 31-34 are objected to.

However, in view of the above claim amendments, this ground of rejection is deemed moot.

The specification stands objected to.

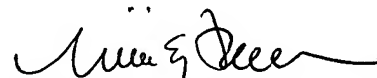
However, attached to this response is a Substitute Specification which meets the requirements of 37 CFR 1.77(b).

CONCLUSION

Accordingly, in view of all of the above, it is believed that this application is now in condition for allowance. Early notice to this effect is earnestly solicited.

Applicant hereby petitions for the Commissioner to charge any additional fees or any underpayment of fees which may be required to maintain the pendency of this case or credit any overpayment to Deposit Account No. 14-0112.

Respectfully submitted,
THE NATH LAW GROUP



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NCBI description of
GenBank U95834

Nucleotide

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All Databases

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search Nucleotide

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Format: GenBank FASTA Graphics More Formats ▼

Download ▼

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Links ▼

GenBank: U95834.1

Change Region Shown

Lactococcus lactis putative lipoprotein Nlp3 precursor, gene, partial cds

Customize View

Features Sequence

Pick Primers

Design and test primers for this sequence using Primer-BLAST.

LOCUS LLU95834 945 bp DNA
linear BCT 24-APR-1998
DEFINITION Lactococcus lactis putative lipoprotein Nlp3 precursor, gene, partial cds.
ACCESSION U95834
VERSION U95834.1 GI:3043865
KEYWORDS .
SOURCE Lactococcus lactis subsp. cremoris MG1363
ORGANISM Lactococcus lactis subsp. cremoris MG1363
Bacteria; Firmicutes; Lactobacillales;
Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 945)
AUTHORS Poquet, I., Ehrlich, S.D. and Gruss, A.
TITLE An export-specific reporter designed for gram-positive bacteria:
application to Lactococcus lactis
JOURNAL J. Bacteriol. 180 (7), 1904-1912 (1998)
PUBMED 9537391
REFERENCE 2 (bases 1 to 945)
AUTHORS Poquet, I. and Gruss, A.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-1997) Laboratoire de Genetique Appliquee-URLGA,
Institut National de la Recherche Agronomique,
CRJ, Jouy en Josas
78352, France
FEATURES Location/Qualifiers
source 1..945
/organism="Lactococcus lactis subsp. cremoris MG1363"
/mol_type="genomic DNA"
/strain="MG1363"
/db_xref="taxon:416870"
complement(<1..330)
/note="identified as a fusion to a signal peptide-less reporter which S. pneumoniae adhesion protein, Swiss-Prot Accession Number P42363"

Recent Activity

Turn Off Clear

Lactococcus lactis
putative lipoprotein

U95834 (1) Nucleotide

All links from this record

Full text in PMC

Protein

PubMed

Taxonomy

Related Sequences

```

/codon_start=1
/transl_table=11
/product="putative lipoprotein Nlp3
precursor"
/protein_id="AAC14602.1"
/db_xref="GI:3043866"
/translation="MKKILMLFAIPAVLLLAGCQKTADKP
EVVTTFEPMYEFTKAIVG
DKVKIENIVPANQEVHEFEPsAKQVATMTNAQAIYNSDDLEKWALKVNNKGVKIEAS
KDVNKKIG"
sig_peptide complement(277..330)
/ note="encodes lipoprotein-type signal
peptide"
mat_peptide complement(<1..276)
/product="putative lipoprotein Nlp3"
ORIGIN
1 tcctttaatt ttattgacat ctttgcttgc ttctattttg
actcctttat tattcacttt
61 cagagcccat ttttcaaggc catcagaatt ataaataata
gcttgagcat ttgtcattgt
121 tgcaacttgc ttggcactcg gttcaaattc gtgaacttct
tgattcgccg gaacaatatt
181 ttcaatttta accttatctc caacaatcgc tttcgtaaat
tcatacatcg gctcaaaagt
241 tgtcacaact tctggtttgc ctgctgtttt ttgacaacca
gcaagaagta aaactgccgg
301 aatagcaaat aacatcaata ttttcttcat cgaaactcct
ccgtaagtac tgataagaat
361 tgacttatca ctttttggtc ttcgtcagta aatttgtctc
ctaattcttg gtaggtactt
421 agagttttct catgatgagc agcatgttct ttagcaactg
gaattgcttt ttctgtcagg
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atttaatcag ttcttgctct
541 tgtaattttt tgagagcttt agttaccgct gctggcgaaa
tcttgagttg ctgggaatt
601 ctgcggttg tcgaaacctc tgcagctaga atcattaaga
tatgttcttg cgtgcttggt
661 agcttaacat tactttngca ttcgccgagt aatatttcat
gcttggtttt tgcaaactgc
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781 taattagttt actggttaat tatatagcaa agtaaaaata
atgtcaacca gttacatta
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ccgaacatca aaacaataag
901 ttttattact aacagtttga ccaccgctag ttgaaccagc tgaca
//

```


BLAST Basic Local Alignment Search Tool

[Edit](#) and [Resubmit](#) [Save Search](#) [Strategies](#) [Formatting options](#) [Download](#)

gb|AAK06214| (145 letters)

Results for: [gb|AAK06214.1 zinc transport transcriptional regulator \[Lactococcus lactis subsp. lactis II1403\]\(145aa\)](#)
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|12725171|gb|AAK06214.1|AE006439_11

Description

zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403]

Molecule type

amino acid

Query Length

145

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

[Reference - compositional score matrix adjustment](#)

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.
Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,739,991,458
Number of sequences	7,946,514
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041
H	0.32399	0.14

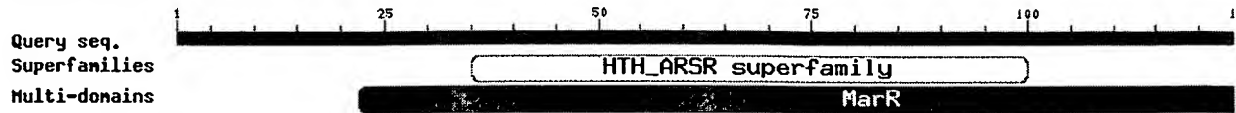
Results Statistics

Length adjustment 109
 Effective length of query 36
 Effective length of database 1873821432
 Effective search space 67457571552
 Effective search space used 67457571552

Graphic Summary

Show Conserved Domains

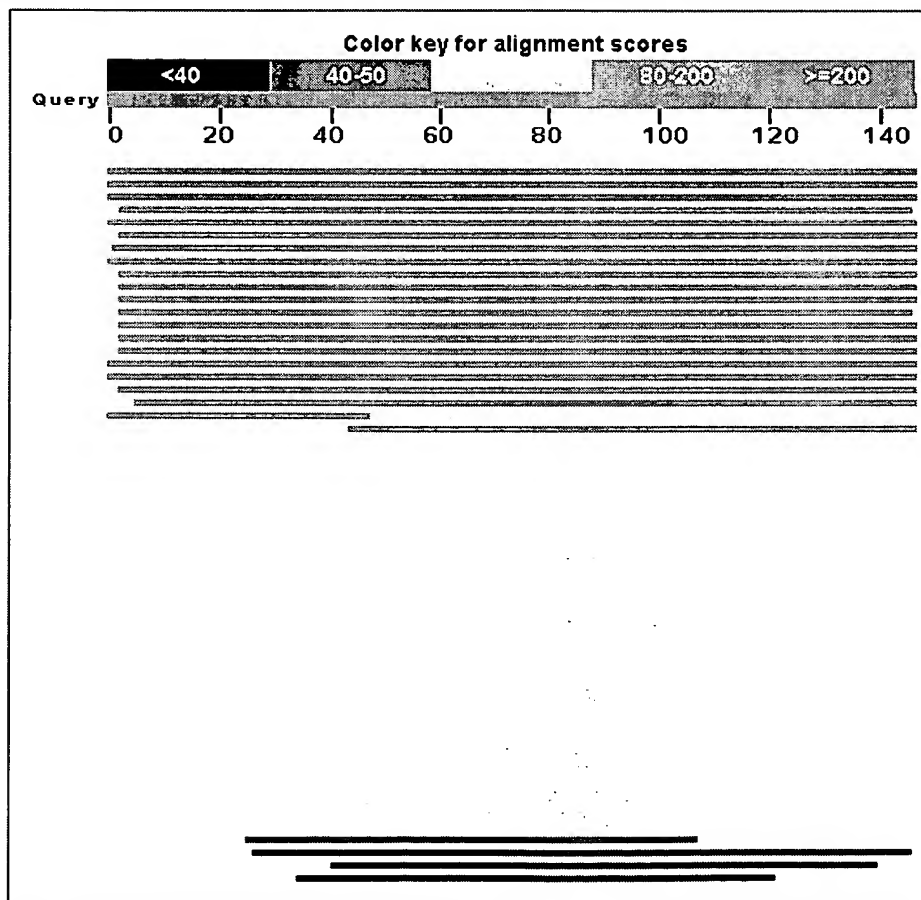
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Sequences producing significant alignments:		Score (Bits)	E Value	
ref NP_268273.1	zinc transport transcription regulator (Lact...	291	1e-77	G
ref YP_011979.1	transcriptional regulator (Lactococcus lacti...	268	1e-70	G
ref YP_001033643.1	transcriptional regulator of the zit oper...	267	2e-70	G
ref YP_001034147.1	multiple antibiotic resistance operon tra...	154	2e-36	G
ref NP_722293.1	putative transcriptional regulator [Streptoc...	145	1e-33	G
ref YP_002122498.1	transcriptional repressor AdcR for Zn(2+)...	143	3e-33	G
ref NP_606407.1	putative repressor protein [Streptococcus py...	141	1e-32	G
ref ZP_02920034.1	hypothetical protein STRINF_00865 [Strepto...	141	2e-32	
ref NP_268489.1	putative repressor protein [Streptococcus py...	141	2e-32	G
ref YP_002551480.1	MarR-family regulatory protein [Streptoco...	138	1e-31	G
ref NP_687190.1	adc operon repressor AdcR [Streptococcus aga...	136	5e-31	G
ref YP_001451205.1	repressor protein adcR [Streptococcus gor...	133	4e-30	G
ref YP_01817760.1	adc operon repressor AdcR [Streptococcus p...	132	6e-30	
ref NP_558569.1	adc operon repressor AdcR [Streptococcus pne...	131	2e-29	G
ref NP_546556.1	adc operon repressor AdcR [Streptococcus pne...	130	2e-29	
ref YP_138725.1	zinc transport transcriptional repressor (St...	129	5e-29	G
ref YP_013746.1	zinc transport transcriptional repressor (St...	128	1e-28	G
ref YP_001197479.1	transcriptional regulator [Streptococcus ...	116	7e-25	G
ref ZP_03625068.1	transcriptional regulator, MarR family [St...	110	4e-23	
emb CAA75313.1	hypothetical protein [Lactococcus lactis subs...	92.4	1e-17	
ref ZP_00365499.1	COG1846: Transcriptional regulators [Strep...	90.9	3e-17	
ref YP_001485459.1	MarR family transcriptional regulator [Ba...	67.0	5e-10	G
ref YP_001189672.1	transcriptional regulator [Streptococcus ...	63.2	6e-09	G
ref YP_187315.1	MarR family transcriptional regulator [Staph...	63.2	7e-09	G
ref YP_001777325.1	transcriptional repressor for Zn(2+)-resp...	62.8	8e-09	G
ref YP_001777.1	hypothetical protein SAOUHSC_02819 [Staphylo...	62.8	8e-09	G
ref ZP_03563431.1	MarR family transcriptional regulator [Sta...	61.2	3e-08	
ref YP_174460.1	MarR family transcriptional regulator [Bacil...	60.5	4e-08	G
ref ZP_080661.1	transcriptional regulator Yvna [Bacillus lic...	59.3	1e-07	G
ref YP_254603.1	hypothetical protein pSHaeC05 [Staphylococcu...	59.3	1e-07	G
ref YP_093087.1	Yvna [Bacillus licheniformis ATCC 14580] >gb...	59.3	1e-07	G
ref ZP_00728634.1	Transcriptional regulator, MarR family [Ba...	55.8	9e-07	
ref ZP_02613091.1	transcriptional regulator, MarR family [Cl...	54.3	3e-06	
ref YP_001263547.1	MarR family transcriptional regulator [Cl...	54.3	3e-06	G
ref YP_001780642.1	MarR family transcriptional regulator [Cl...	54.3	3e-06	G
ref YP_001033131.1	MarR family transcriptional regulator [La...	53.9	4e-06	G
ref ZP_02617530.1	transcriptional regulator, MarR family [Cl...	53.9	4e-06	
ref YP_861360.1	MarR family transcriptional regulator [Grame...	53.9	4e-06	G
ref NP_391388.1	hypothetical protein BSU35080 [Bacillus subt...	53.5	5e-06	G
ref ZP_02994615.1	hypothetical protein CLOSP0_01734 [Clostri...	53.5	6e-06	
ref ZP_01994138.1	hypothetical protein DORLON_00120 [Dorea l...	53.1	6e-06	
ref ZP_03294054.1	hypothetical protein CLOHIR_02015 [Clostri...	53.1	7e-06	
ref ZP_02511326.1	hypothetical protein CLOBAR_00939 [Clostri...	52.4	1e-05	
ref YP_001390364.1	MarR family transcriptional regulator [Cl...	52.4	1e-05	G
ref YP_001786407.1	MarR family transcriptional regulator [Cl...	51.6	2e-05	G
ref YP_505725.1	transcriptional regulator [Lactococcus lacti...	51.2	2e-05	G
ref YP_001699048.1	MarR family transcriptional regulator [Ly...	51.2	3e-05	G
ref NP_266864.1	transcription regulator [Lactococcus lactis ...	51.2	3e-05	G
ref ZP_01723095.1	transcriptional regulator, MarR family pro...	50.4	4e-05	
ref YP_808147.1	transcriptional regulator [Lactococcus lacti...	50.4	5e-05	G
ref NP_786298.1	transcription regulator [Lactobacillus plant...	50.1	6e-05	G
ref YP_757477.1	MarR family transcriptional regulator [Maric...	50.1	6e-05	G
ref NP_391385.1	hypothetical protein BSU35050 [Bacillus subt...	50.1	6e-05	G
ref NP_111681.1	transcription regulator (SlyA-related) [Ther...	49.7	7e-05	G
ref NP_419015.1	MarR family transcriptional regulator [Caulo...	49.3	9e-05	G
ref YP_001031492.1	MarR family transcriptional regulator [La...	49.3	1e-04	G
ref NP_603575.1	MarR family transcriptional regulator [Fusob...	48.9	1e-04	G
ref YP_136915.1	MarR family transcriptional regulator [Strep...	48.9	1e-04	G
ref YP_000165566.1	possible MarR family transcriptional regu...	48.9	1e-04	G
ref ZP_00144671.1	Transcriptional regulator, MarR family [Fu...	48.9	1e-04	G

ref YP_819912.1	MarR family transcriptional regulator [Strep...	48.9	1e-04	G
ref YP_079349.1	transcriptional regulator Yvmb [Bacillus lic...	48.5	2e-04	G
ref ZP_01219553.1	putative transcriptional regulator, MarR f...	45.1	2e-04	
ref YP_091755.1	Yvmb [Bacillus licheniformis ATCC 14580] >gb...	45.1	2e-04	G
ref YP_129221.1	MarR family transcriptional regulator [Photo...	45.1	2e-04	G
ref ZP_00990845.1	hypothetical transcriptional regulator, Ma...	48.1	2e-04	
ref YP_091319891.1	MarR family transcriptional regulator [Al...	47.8	3e-04	G
ref YP_091838202.1	MarR family transcriptional regulator [Le...	47.8	3e-04	G
ref YP_106811.1	putative transcriptional regulatory protein ...	47.4	4e-04	G
ref YP_091861850.1	Transcriptional regulator, marR family [L...	47.4	4e-04	G
ref YP_091310724.1	MarR family transcriptional regulator [Cl...	47.4	4e-04	G
ref ZP_01065869.1	hypothetical transcriptional regulator, Ma...	47.0	5e-04	
ref YP_140799.1	MarR family transcriptional regulator [Strep...	47.0	5e-04	G
ref YP_143999.1	MarR family transcriptional regulator [Therm...	46.6	6e-04	G
ref YP_283371.1	regulatory protein, MarR [Ralstonia eutropha...	46.6	7e-04	G
ref YP_091307422.1	MarR family transcriptional regulator [Cl...	46.6	7e-04	G
ref ZP_02950515.1	transcriptional regulator, MarR family [Cl...	46.2	8e-04	
ref NP_268269.1	transcription regulator [Lactococcus lactis ...	46.2	0.001	G
ref YP_092352539.1	transcriptional regulator, MarR family [D...	46.2	0.001	G
ref ZP_01689435.1	probable marR-family transcription regulat...	46.2	0.001	
ref YP_773250.1	MarR family transcriptional regulator [Burkh...	45.8	0.001	G
ref ZP_01131766.1	transcriptional regulator, MarR family pro...	45.8	0.001	
ref ZP_00238819.1	transcriptional regulator, MarR family [Ba...	45.6	0.001	
ref YP_092467440.1	transcriptional regulator, MarR family [C...	45.6	0.001	G
ref ZP_02547491.1	hypothetical protein BLAHAN_01259 [Blautia...	45.4	0.001	
ref ZP_02891041.1	transcriptional regulator, MarR family [Bu...	45.4	0.001	
ref YP_091808132.1	MarR family transcriptional regulator [Bu...	45.4	0.001	G
ref ZP_02906301.1	transcriptional regulator, MarR family [Bu...	45.4	0.001	
ref ZP_02362996.1	transcriptional regulator, MarR family pro...	45.4	0.001	
ref NP_377055.1	MarR family transcriptional regulator [Bacil...	45.4	0.002	G
ref NP_792475.1	MarR family transcriptional regulator [Clostr...	45.4	0.002	G
ref ZP_03570809.1	transcriptional regulator, MarR family [Bu...	45.1	0.002	
ref YP_091119315.1	MarR family transcriptional regulator [Bu...	45.1	0.002	G
ref YP_092418276.1	Histone acetyltransferase HPA2 and relate...	45.1	0.002	G
ref ZP_02355848.1	transcriptional regulator, MarR family pro...	45.1	0.002	
ref YP_443075.1	MarR family transcriptional regulator [Burkh...	44.7	0.002	G
ref ZP_02633646.1	transcriptional regulator, MarR family [Cl...	44.7	0.002	
ref YP_091374721.1	MarR family transcriptional regulator [Ba...	44.7	0.002	G
ref YP_529461.1	transcriptional regulator [Leuconostoc mesen...	44.7	0.002	G
ref ZP_02027445.1	hypothetical protein EUBVEN_02713 [Eubacte...	44.7	0.003	

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>ref|NP_268273.1| **G** zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403]
 gb|AAK06214.1|AE006439_11 **G** zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
 Length=145

GENE ID: 1115793 zitR | zinc transport transcription regulator
 [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 1e-77, Method: Compositional matrix adjust.
 Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

Query	1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL	60
Sbjct	1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL	60
Query	61	KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Sbjct	61	KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Query	121	LGNKFTDEEQEVISKFLSALTEEFQ	145
Sbjct	121	LGNKFTDEEQEVISKFLSALTEEFQ	145

>ref|YP_811979.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 gb|ABJ73866.1| **G** Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=145


GENE ID: 4433026 LACR 2420 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)


Score = 268 bits (685), Expect = 1e-70, Method: Compositional matrix adjust.
Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
          MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct 1  MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMLAAEVSTNARIAEQL 60

Query 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQE 120
          KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHA HHEKTLSTYQE
Sbjct 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHAHHEKTLSTYQE 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
          LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct 121 LGDKFTDEEQKVISQFLSVLTEEFR 145
```

>ref|YP_001033643.1|  transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]

emb|CAL98965.1|  transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145


GENE ID: 4799067 zitR | transcriptional regulator of the zit operon
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)


Score = 267 bits (682), Expect = 2e-70, Method: Compositional matrix adjust.
Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
          MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct 1  MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMLAAEVSTNARIAEQL 60

Query 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQE 120
          KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKA+PVAKEHA HHEKTLSTYQE
Sbjct 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAIPVAKEHAHHEKTLSTYQE 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
          LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct 121 LGDKFTDEEQKVISQFLSVLTEEFR 145
```

>ref|YP_001034147.1|  multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]

gb|ABN43597.1|  Multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
Length=147


GENE ID: 4806188 adcR | multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
(10 or fewer PubMed links)


Score = 154 bits (389), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 78/142 (54%), Positives = 102/142 (71%), Gaps = 0/142 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          LA +IDQFL ++ AEN+HEIL+G C SDV LT+TQEHILMLL+E+ TN+ +A+KL +
Sbjct 4  LAQKIDQFLNEVILKAENQHEILIGSCTSDVPLTNTQEHILMLLSEESLTNSDLAKKLVN 63

Query 63  SPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L QE++++ + D RV + LTE A P+AKEH HH TL TYQ+L
Sbjct 64  SQAAVTKAVKSLARQEMLQAFKDKRDARVTFYRLTELAQPIAKEHQHHHAHTLETYQKLA 123

Query 123 NKFTDEEQEVISKFLSALTEEF 144
          +F+ EQ VI+KFL AL E
Sbjct 124 EQFSASEQAVIAKFLALVGEI 145
```

>ref|NP_722293.1|  putative transcriptional regulator [Streptococcus mutans UA159]

gb|AAN59599.1|AE015022_6  putative transcriptional regulator [Streptococcus mutans UA159]
Length=148

GENE ID: 1029245 SMU.1995c | putative transcriptional regulator
[Streptococcus mutans UA159] (10 or fewer PubMed links)

Score = 145 bits (365), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 76/146 (52%), Positives = 105/146 (71%), Gaps = 1/146 (0%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQIS-TNAKIAEK 59
          M+L QID + I+ AEN HE+L+G C+SDVKLT+TQEHILMLL+++ S TN+ +A++
Sbjct 1  MTLGQQIDALINQIILKAENHHELLIGSCQSDVKLTNTQEHILMLLSQEKSLTNSDLAKE 60

Query 60  LKISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQ 119
          L IS AAVTKA+K L QE+++ + D RV + LT+ A PVAKEH HH TLS Y
Sbjct 61  LNISQAAVTKAVKSLVQEMLELIKDGTDARVTFYRLTKLAEPVAKEHEHHHVATLSVYD 120

Query 120 ELGNKFTDEEQEVISKFLSALTEEFQ 145
          + KF+ +E+ VIS+FL+ALT+E +
Sbjct 121 RISQKFSQKEKSVISRFLTALTKELE 146
```

>ref|YP_002122498.1| **G** transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]
 gb|ACG61485.1| **G** transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]
 Length=147

GENE ID: 6760627 adcR | transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]

Score = 143 bits (361), Expect = 3e-33, Method: Compositional matrix adjust.
 Identities = 70/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          L ++D + I+ AEN+HE+L G C+SDVKLT+TQEHILMLL+++ TN +A++L I
Sbjct 4  LEKKLDNLVNRILLKAENQHLLFGACQSDVKLTNTQEHILMLLSQEKLNTDLAKRLNI 63

Query 63  SPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L +QE++ ++ T D RV + LT+ A P+AKEH HH+KTL+ Y L
Sbjct 64  SQAAVTKAIKGLIKQEMLAGTKDVTVDARVTFELTDLARPIAKEHTHHHDKTLAVYHRL 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
          F+ EEQ ++ KF++A +EE +
Sbjct 124 AHFSAEEQVIVEKFITAFSEELE 146
```

>ref|NP_606407.1| **G** putative repressor protein [Streptococcus pyogenes MGAS8232]
 ref|NP_663873.1| **G** putative repressor protein [Streptococcus pyogenes MGAS315]
 ref|NP_801332.1| **G** putative repressor protein [Streptococcus pyogenes SSI-1]
 20 more sequence titles

ref|YP_059443.1| **G** MarR family transcriptional regulator [Streptococcus pyogenes MGAS10394]
 ref|YP_279544.1| **G** MarR family transcriptional regulator [Streptococcus pyogenes MGAS6180]
 ref|YP_595809.1| **G** MarR family transcriptional regulator [Streptococcus pyogenes MGAS9429]
 ref|YP_597688.1| **G** MarR family transcriptional regulator [Streptococcus pyogenes MGAS10270]
 ref|YP_599676.1| **G** MarR family transcriptional regulator [Streptococcus pyogenes MGAS2096]
 ref|YP_601578.1| **G** Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10750]
 ref|YP_001127671.1| **G** MarR family regulatory protein [Streptococcus pyogenes str. Manfredo]
 ref|YP_002285129.1| **G** Putative repressor protein [Streptococcus pyogenes NZ131]
 sp|Q5XEA3.1|ADCR STRP6 RecName: Full=Transcriptional repressor adcR
 gb|AAL96906.1| **G** putative repressor protein [Streptococcus pyogenes MGAS8232]
 gb|AAM78676.1| **G** putative repressor protein [Streptococcus pyogenes MGAS315]
 dbj|BAC63165.1| **G** putative repressor protein [Streptococcus pyogenes SSI-1]
 gb|AAT86260.1| **G** Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10394]
 gb|AAX71189.1| **G** transcriptional regulator, MarR family [Streptococcus pyogenes MGAS6180]
 gb|ABF31265.1| **G** transcriptional regulator, MarR family [Streptococcus pyogenes MGAS9429]
 gb|ABF33144.1| **G** Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10270]
 gb|ABF35132.1| **G** Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS2096]
 gb|ABF37034.1| **G** Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10750]
 emb|CAM29417.1| **G** MarR-family regulatory protein [Streptococcus pyogenes str. Manfredo]
 gb|ACI60434.1| **G** Putative repressor protein [Streptococcus pyogenes NZ131]
 Length=147

GENE ID: 994164 adcR | putative repressor protein [Streptococcus pyogenes MGAS8232] (10 or fewer PubMed links)

Score = 141 bits (356), Expect = 1e-32, Method: Compositional matrix adjust.
 Identities = 69/144 (47%), Positives = 101/144 (70%), Gaps = 0/144 (0%)

```
Query 2  SLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLK 61
          +L ++D + TI+ AEN+HE+L G C+SDVKLT+TQEHILMLL++Q TN +A+ L
Sbjct 3  TLEKKLDNLVNTILLKAENQHLLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALN 62

Query 62  ISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL 121
          IS AAVTKA+K L +Q+++ ++ T D RV + LTE A P+A EH HH++TL+ Y L
Sbjct 63  ISQAAVTKAIKSLVKQDMLAGTKDVTVDARVTFELTELAKPIASEHTHHHDETLNVYNRL 122

Query 122 GNKFTDEEQEVISKFLSALTEEFQ 145
          KF+ +E E++ KF++ EE +
Sbjct 123 LQKFSAKELEIVDKFVTVFAEELE 146
```

>ref|ZP_02920004.1| hypothetical protein STRINF_00865 [Streptococcus infantarius]





subsp. infantarius ATCC BAA-102] " ' .
 gb|EDT48012.1| hypothetical protein STRINF_00865 [Streptococcus infantarius
 subsp. infantarius ATCC BAA-102]
 Length=148

Score = 141 bits (355), Expect = 2e-32, Method: Compositional matrix adjust.
 Identities = 70/145 (48%), Positives = 103/145 (71%), Gaps = 0/145 (0%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
          M L QID + I+ AEN+HE+L G C+S V+LT+TQEHILMLL+++ TN+ +A++L
Sbjct 1  MQLEKQIDCLVNEILLKAENQHELLFGACQSGVELTNTQEHILMLLSQERLTNSALAKRL 60

Query 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQE 120
          IS AAVTKA+K L ++ ++ + +D RV + LTE A PVA EH HH TLS Y++
Sbjct 61  NISQAAVTKAIKCLVKEGMLAPVKNKDDARVTFELTEFAKPVADENHHHHHATLSVYKK 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
          + + F+DEEQ +IS+FL+A ++E +
Sbjct 121 MIDDFSDEEQSIISRFLTAFSDELE 145
```

>ref|NP_268489.1|  putative repressor protein [Streptococcus pyogenes M1 GAS]
 ref|YP_281441.1|  MarR family transcriptional regulator [Streptococcus pyogenes
 MGAS5005]
 gb|AAK33210.1|  putative repressor protein [Streptococcus pyogenes M1 GAS]
 gb|AAZ50696.1|  transcriptional regulator, MarR family [Streptococcus pyogenes
 MGAS5005]
 Length=147



GENE ID: 900432 adcR | putative repressor protein
 [Streptococcus pyogenes M1 GAS] (10 or fewer PubMed links)

Score = 141 bits (355), Expect = 2e-32, Method: Compositional matrix adjust.
 Identities = 69/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          L ++D + TI+ AEN+HE+L G C+SDVKLT+TQEHILMLL++Q TN +A+ L I
Sbjct 4  LEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQLTNTDLAKALNI 63

Query 63  SPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L +Q+++ ++ T D RV + LTE A P+A EH HH++TL+ Y L
Sbjct 64  SQAAVTKAIKSLVKQDMLAGTKDVTVDARVTFELTELAKPIASEHTHHHDETLNVYNRL 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
          KF+ +E E++ KF++ EE +
Sbjct 124 QKFSAKELEIVDKFVTVFAEELE 146
```

>ref|YP_002561480.1|  MarR-family regulatory protein [Streptococcus uberis 0140J]
 emb|CAR40515.1|  MarR-family regulatory protein [Streptococcus uberis 0140J]
 Length=147




GENE ID: 7392663 SUB0110 | MarR-family regulatory protein
 [Streptococcus uberis 0140J]




Score = 138 bits (348), Expect = 1e-31, Method: Compositional matrix adjust.
 Identities = 69/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          L ++IDQ + I+ AEN+HE+L G C+S VKLT+TQEHILMLL+++ TN +A+KL I
Sbjct 4  LESKIDQLVNIQLLKAENQHELLFGACQSHVKTNTQEHILMLLSQEQLTNTDLAKKLNI 63

Query 63  SPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L + E++ + + T D RV + LT A P+A+EH HH++TL+ Y +L
Sbjct 64  SQAAVTKAIKSLMKHEMLSAIKDVTVDARVTFELTPAAKPIAEHHTQHHDDETLNVYTKLL 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
          + F+ EE+ VI KFL+ ++E +
Sbjct 124 SSFSSEEKAVIDKFLTVFSDELE 146
```

>ref|NP_687190.1|  adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
 ref|NP_734620.1|  adc operon repressor AdcR [Streptococcus agalactiae NEM316]
 ref|YP_328885.1|  adc operon repressor AdcR [Streptococcus agalactiae A909]
 13 more sequence titles

ref|ZP_00781732.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
 ref|ZP_00784062.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
 ref|ZP_00786322.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
 ref|ZP_00787320.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
 ref|ZP_00790981.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
 gb|AAM99062.1|AE014198_10  adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
 emb|CAD45795.1|  unknown [Streptococcus agalactiae NEM316]
 gb|ABA46120.1|  adc operon repressor AdcR [Streptococcus agalactiae A909]
 gb|EAO61676.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
 gb|EAO70283.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
 gb|EAO73974.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
 gb|EAO74935.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
 gb|EAO77202.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
 Length=147

GENE ID: 1012928 adcR | adc operon repressor AdcR
[*Streptococcus agalactiae* 2603V/R] (10 or fewer PubMed links)

Score = 136 bits (343), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 65/143 (45%), Positives = 99/143 (69%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          L ++D + I+ AEN+HE+L G C+SDVKLT+TQEHILMLL+++ TN+ +A+KL I
Sbjct 4  LEQKLDHLVLSQILLKAENQHELLFGTCQSDVKLTNTQEHILMLLSQEQLTNSDLAKKLNI 63

Query 63  SPAAVTKALKKLQEQELIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L Q+++K+++ + D R+ + L+E A P+A EH HH+ TL Y L
Sbjct 64  SQAAVTKAVKSLISQDMLKANKDSKDARITYFELSELAKPIADEHTHHHDNTLGVYGRLV 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
          N F+ +E+ V+ +FL + E +
Sbjct 124 NHFSKDEKVVLERFLDLFSRELE 146
```

>ref|YP_001451205.1| **G** repressor protein adcR [*Streptococcus gordonii* str. Challis substr. CH1]
gb|AAO43167.1| putative transcriptional repressor; AdcR [*Streptococcus gordonii* subsp. challis]
gb|ABV10972.1| **G** repressor protein adcR [*Streptococcus gordonii* str. Challis substr. CH1]
Length=147

GENE ID: 5599115 adcR | repressor protein adcR
[*Streptococcus gordonii* str. Challis substr. CH1] (10 or fewer PubMed links)

Score = 133 bits (335), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 75/142 (52%), Positives = 101/142 (71%), Gaps = 0/142 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          LA++ID FL I+ AEN+HEIL+G C S+V LT+TQEHILMLLAE++ TN+ +A+KL +
Sbjct 4  LAHKIDSFLNEIILKAENQHAILVGSCSTNVALTNTQEHILMLLAEMLTNSDLAKKLNV 63

Query 63  SPAAVTKALKKLQEQELIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L Q +++++ + D RV + LTE A P+A EH HH TL TYQ L
Sbjct 64  SQAAVTKAVKSLINQGMLETFKDKKDARVTFYRLTELAQPIADEHEHHHAHTLETYQSLL 123

Query 123 NKFTDEEQEVISKFLSALTEEF 144
          ++F+ +EQ+ I KFL AL E
Sbjct 124 DRFSQDEQQAIEKFLEALVGEI 145
```

>ref|ZP_01817760.1| adc operon repressor AdcR [*Streptococcus pneumoniae* SP3-BS71]
ref|YP_002512031.1| **G** MarR-family regulatory protein [*Streptococcus pneumoniae* ATCC 700669]
gb|EDK74363.1| adc operon repressor AdcR [*Streptococcus pneumoniae* SP3-BS71]
emb|CAR69937.1| **G** MarR-family regulatory protein [*Streptococcus pneumoniae* ATCC 700669]
Length=146

Score = 132 bits (333), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 71/143 (49%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          LA ID FL ++ AEN+HEIL+G C S+V LT+TQEHILMLL+E+ TN+++A +L +
Sbjct 4  LAKDIDAFLNEVILQAENQHAILGHCTSEVALTNTQEHILMLLSESLTNSELARRLNV 63

Query 63  SPAAVTKALKKLQEQELIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH HHE TL TY+++
Sbjct 64  SQAAVTKAIKSLVKEGMLETSSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
          +FT EQ+VI +FL+AL E +
Sbjct 124 TQFTPNEQKVIQRFLTALVGEIK 146
```

>ref|NP_359569.1| **G** adc operon repressor AdcR [*Streptococcus pneumoniae* R6]
ref|ZP_01825537.1| Transcriptional repressor for Zn(2+)-responsive expression [*Streptococcus pneumoniae* SP11-BS70]
ref|YP_001836857.1| **G** adc operon repressor AdcR [*Streptococcus pneumoniae* CGSP14]
ref|ZP_02964427.1| putative transcriptional repressor [*Streptococcus pneumoniae* CDC0288-04]
gb|AAL00780.1| **G** Transcriptional repressor for Zn(2+)-responsive expression [*Streptococcus pneumoniae* R6]
gb|EDK63077.1| Transcriptional repressor for Zn(2+)-responsive expression [*Streptococcus pneumoniae* SP11-BS70]
gb|ACB91392.1| **G** adc operon repressor AdcR [*Streptococcus pneumoniae* CGSP14]
gb|EDT94590.1| putative transcriptional repressor [*Streptococcus pneumoniae* CDC0288-04]
Length=166

GENE ID: 933868 adcR | adc operon repressor AdcR [*Streptococcus pneumoniae* R6]
(10 or fewer PubMed links)

Score = 131 bits (329), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
```


Sbjct	24	LA I+ FL ++ AEN+HEIL+G C S+V LT+TQEHILMLL+E+ TN+++A +L + LAKDINAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV	83
Query	63	SPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTKAVPVAKETHHHEKTLSTYQELG S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH HHE TL TY+++	122
Sbjct	84	SQAAVTKAIKSLVKEGMLKSKDSKARVIFYQLTDLARPIAEHHHHHEHTLLTYEQVA	143
Query	123	NKFTDEEQEVISKFLSALTEEFQ +FT EQ+VI +FL+AL E +	145
Sbjct	144	TQFTPNEQKVIQRFLTALVGEIK	166

>ref|NP_346586.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]
 ref|ZP_01408975.1| **G** hypothetical protein SpneT_02000553 [Streptococcus pneumoniae TIGR4]
 ref|YP_817386.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae D39]
 29 more sequence titles

ref|ZP_01820229.1| adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
 ref|ZP_01821749.1| adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
 ref|ZP_01827937.1| adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
 ref|ZP_01830531.1| adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
 ref|ZP_01833186.1| adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
 ref|ZP_01835060.1| adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
 ref|ZP_02708953.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1873-00]
 ref|ZP_02710784.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1087-00]
 ref|ZP_02713441.1| putative transcriptional repressor [Streptococcus pneumoniae SP195]
 ref|ZP_02718213.1| putative transcriptional repressor [Streptococcus pneumoniae CDC3059-06]
 ref|ZP_02721950.1| putative transcriptional repressor [Streptococcus pneumoniae MLV-016]
 ref|YP_001695528.1| **G** putative transcriptional repressor [Streptococcus pneumoniae Hungary19A-6]
 ref|YP_002038763.1| **G** transcriptional regulator, MarR family [Streptococcus pneumoniae G54]
 emb|CAA96184.1| AdcR protein [Streptococcus pneumoniae]
 gb|AAK76226.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]
 gb|ABJ54931.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae D39]
 gb|EDK65765.1| adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
 gb|EDK68416.1| adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
 gb|EDK70926.1| adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
 gb|EDK76701.1| adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
 gb|EDK80035.1| adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
 gb|EDK81745.1| adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
 gb|ACA36761.1| **G** putative transcriptional repressor [Streptococcus pneumoniae Hungary19A-6]
 gb|EDT50754.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1873-00]
 gb|EDT91227.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1087-00]
 gb|EDT92758.1| putative transcriptional repressor [Streptococcus pneumoniae SP195]
 gb|EDT96372.1| putative transcriptional repressor [Streptococcus pneumoniae CDC3059-06]
 gb|EDT98576.1| putative transcriptional repressor [Streptococcus pneumoniae MLV-016]
 gb|ACF56415.1| **G** transcriptional regulator, MarR family [Streptococcus pneumoniae G54]
 Length=146

GENE ID: 931929 SP 2172 | adc operon repressor AdcR
 [Streptococcus pneumoniae TIGR4] (10 or fewer PubMed links)
 Score = 130 bits (328), Expect = 2e-29, Method: Compositional matrix adjust.
 Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

Query	3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI	62
Sbjct	4	LA I+ FL ++ AEN+HEIL+G C S+V LT+TQEHILMLL+E+ TN+++A +L + LAKDINAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV	63
Query	63	SPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTKAVPVAKETHHHEKTLSTYQELG S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH HHE TL TY+++	122
Sbjct	64	SQAAVTKAIKSLVKEGMLKSKDSKARVIFYQLTDLARPIAEHHHHHEHTLLTYEQVA	123
Query	123	NKFTDEEQEVISKFLSALTEEFQ +FT EQ+VI +FL+AL E +	145
Sbjct	124	TQFTPNEQKVIQRFLTALVGEIK	146

>ref|YP_138725.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus LMG 183T1]
 ref|YP_140614.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus CNR21066]
 gb|AAV59910.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus LMG 18311]
 gb|AAV61799.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus CNR21066]

Length=151

GENE ID: 3164452 *adcR* | zinc transport transcriptional repressor
[*Streptococcus thermophilus* LMG 18311] (10 or fewer PubMed links)

Score = 129 bits (325), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 62/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
          + L Q++Q + I+ AEN++E+L+G+C S VKLT+TQEHILMLL+E TN+++A+ L
Sbjct 6  IELEEQVNQLINQILLKAENQYELLIGQCRSKVKLTNTQEHILMLLSEGQKTNSELAKAL 65

Query 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
          +S AAVTKA+K L ++ +++ + +D RV + LT++A P+A+EH HH++TL Y+
Sbjct 66  NVSQAAVTKAVKTLVKEGMLLEGKKDKDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS 125

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
          + ++F +E++VI +FL L E+ +
Sbjct 126 VLDQFDHQERQVIGRFLIKLAEKIE 150
```

>ref|YP_819746.1| **G** zinc transport transcriptional repressor [*Streptococcus thermophilus* LMD-9]

gb|ABJ65550.1| **G** transcriptional regulator, MarR family [*Streptococcus thermophilus* LMD-9]
Length=147

GENE ID: 4438531 *STER 0233* | zinc transport transcriptional repressor
[*Streptococcus thermophilus* LMD-9] (10 or fewer PubMed links)

Score = 128 bits (322), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 61/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
          + L +++Q + I+ AEN++E+L+G+C S VKLT+TQEHILMLL+E TN+++A+ L
Sbjct 2  IELEERVNQLINQILLKAENQYELLIGQCRSKVKLTNTQEHILMLLSEGQKTNSELAKAL 61

Query 61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
          +S AAVTKA+K L ++ +++ + +D RV + LT++A P+A+EH HH++TL Y+
Sbjct 62  NVSQAAVTKAVKTLVKEGMLLEGKKDKDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS 121

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
          + ++F +E++VI +FL L E+ +
Sbjct 122 VLDQFDHQERQVIGRFLIKLAEKIE 146
```

>ref|YP_001197479.1| **G** transcriptional regulator [*Streptococcus suis* 05ZYH33]

gb|ABP89079.1| **G** Transcriptional regulator [*Streptococcus suis* 05ZYH33]
Length=149

GENE ID: 5099418 *SSU05 0109* | transcriptional regulator
[*Streptococcus suis* 05ZYH33] (10 or fewer PubMed links)

Score = 116 bits (290), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

```
Query 3  LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
          +A +I+++L I+ +EN+ EIL+G C+S VKLT+TQEHILML+ + TN +IA++L +
Sbjct 6  IALEIEKYLHEIVLSSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAAYTNTEIAKELNV 65

Query 63  SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
          S AA+TKA K L Q L+ + R D R+V +SLTE A P+A EHA HH TL Y+EL
Sbjct 66  SQAATKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAHHHAHTLEAYEELL 125

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
          ++ EEQE I++FLS L E+ +
Sbjct 126 ENYSLEEQESIAFLSELVEKIR 148
```

>ref|ZP_03625066.1| transcriptional regulator, MarR family [*Streptococcus suis* 89/1591]

gb|EEF54628.1| transcriptional regulator, MarR family [*Streptococcus suis* 89/1591]
Length=149

Score = 110 bits (275), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 69/140 (49%), Positives = 98/140 (70%), Gaps = 0/140 (0%)

```
Query 6  QIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPA 65
          +I+++L I+ +EN+ EIL+G C+S VKLT+TQEHILML+ + TN +IA++L +S A
Sbjct 9  EIEKYLHEIVLSSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAAYTNTEIAKELNVSA 68

Query 66  AVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKF 125
          A+TKA K L Q L+ + R D R+V +SLTE A P+A EHA HH TL Y+EL +
Sbjct 69  AITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIATEHAHHHAHTLEAYEELLEHY 128

Query 126 TDEEQEVISKFLSALTEEFQ 145
          + EEQE I++FLS L E+ +
Sbjct 129 SLEEQESIAFLSELVEKIR 148
```

>emb|CAA75313.1| hypothetical protein [*Lactococcus lactis* subsp. *cremoris*]
Length=48

Score = 92.4 bits (228), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 43/47 (91%), Positives = 46/47 (97%), Gaps = 0/47 (0%)



Query 1 MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLA 47
 MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA
 Sbjct 1 MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILA 47

>ref|ZP_00365496.1| COG1846: Transcriptional regulators [Streptococcus pyogenes M49 591]
 Length=103

Score = 90.9 bits (224), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 45/102 (44%), Positives = 68/102 (66%), Gaps = 0/102 (0%)

Query 44 MLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPV 103
 MLL++Q TN ++L IS AAVTKA+K L +Q+++ ++ T D RV + LTE A P+
 Sbjct 1 MLLSQQLRTNTDLAKALNISQAAVTKA+KSLVKQDMLAGTKDVTVDARVTFELTELAKPI 60

Query 104 AKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 A EH HH++TL+ Y L KF+ +E E++ KF++ EE +
 Sbjct 61 ASEHTHHHDETLNVYNRLQKFSAKELEIVDKFVTVFAEELE 102



>ref|YP_001485459.1|  MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
 ref|ZP_03056081.1| Yvna [Bacillus pumilus ATCC 7061]
 gb|ABV60899.1|  possible MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
 gb|EDW20313.1| Yvna [Bacillus pumilus ATCC 7061]
 Length=152

GENE ID: 5619427 BPUM_0200 | MarR family transcriptional regulator
 [Bacillus pumilus SAFR-032] (10 or fewer PubMed links)

Score = 67.0 bits (162), Expect = 5e-10, Method: Compositional matrix adjust.
 Identities = 40/111 (36%), Positives = 66/111 (59%), Gaps = 2/111 (1%)

Query 36 TSTQEHILMLLAEQI--STNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVL 93
 T TQ HIL ++ S N ++++LK+S A+TKA+KKL ++ ++ D++ V
 Sbjct 42 TLTQLHILSMIQANPNESNNTFLSQQLKLSKPAITKAVKKLIDKGMVDYCHRGDKKSVY 101

Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 +SLTEK +A H HEK +++Y E +F ++E +VI +FL A E+
 Sbjct 102 YSLTEKGTQLAALHDELHEKAVASYLEFLQQFHEDELQVIERFLKAWKEKI 152








>ref|YP_001199672.1|  transcriptional regulator [Streptococcus suis 98HAH33]
 gb|ABP91272.1|  Transcriptional regulator [Streptococcus suis 98HAH33]
 Length=87

GENE ID: 5101832 SSU98_0112 | transcriptional regulator
 [Streptococcus suis 98HAH33] (10 or fewer PubMed links)

Score = 63.2 bits (152), Expect = 6e-09, Method: Compositional matrix adjust.
 Identities = 41/86 (47%), Positives = 56/86 (65%), Gaps = 0/86 (0%)

Query 60 LKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQ 119
 + S AA+TKA K L Q L+ + R D R+V +SLTE A P+A EHA HH TL Y+
 Sbjct 1 MNVSQAAITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAAHHAHTLEAYE 60

Query 120 ELGNKFTDEEQEVISKFLSALTEEFQ 145
 EL ++ EEQE I++FLS L E+ +
 Sbjct 61 ELLENYSLEEQESIARFLSELVEKIR 86

>ref|YP_187318.1|  MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus COL]
 ref|YP_495086.1|  MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300]
 ref|YP_001576367.1|  MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300 TCH1516]
 ref|ZP_02761767.1|  MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300 TCH1516]
 gb|AAW37302.1|  transcriptional regulator, MarR family [Staphylococcus aureus subsp. aureus COL]
 gb|ABD21126.1|  transcriptional regulator, MarR family [Staphylococcus aureus subsp. aureus USA300_FPR3757]
 gb|ABX30488.1|  MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300 TCH1516]
 Length=154

GENE ID: 3238188 SACOL2524 | MarR family transcriptional regulator
 [Staphylococcus aureus subsp. aureus COL] (10 or fewer PubMed links)

Score = 63.2 bits (152), Expect = 7e-09, Method: Compositional matrix adjust.
 Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

Query 35 LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVL 93
 L+ TQ HI+ L+ N K ++E L +S A+TK++KKL ++L+ S ++R V
 Sbjct 36 LSLTQFHIIELIDNNDKVNKFLSEMLNVSKPAITKSIKKLLAKDLVESHNEFNKREVN 95

Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 +SLT+K ++ H HEK++ Y+E+ F D+E VI +FL+ EE +
 Sbjct 96 YSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDEMAVIIIEFLNRSIEELK 147

>ref|YP_001727325.1| **G** transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]

gb|ACA81881.1| **G** Transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]
Length=146

GENE ID: 6063203 **adcR** | transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20] (10 or fewer PubMed links)

Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 41/138 (29%), Positives = 72/138 (52%), Gaps = 2/138 (1%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
MS ++ I Q L T +Q      E + + + K+ +TQ H+LMLL Q +TN+ +AE +
Sbjct 1  MSQSDHIIQEINTFVQTYAASSEFI--QTAAQKINATQAHLLMLLKTQHATNSSLAESM 58

Query 61  KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
++ A+TKA+K L      + +++ ND+R V + L+ + + +A +H      H
Sbjct 59  HLTKPAITKAIKNLIAHGYVVATKDVNDKRSVNYQLSTEGMLAAQHEASHRNLHHRIDH 118

Query 121  LGNKFTDEEQEVISKFLS 138
FT ++E I FL+
Sbjct 119  TIATFTPAQRETIVAFLA 136
```

>ref|YP_501277.1| **G** hypothetical protein SAOUHSC_02819 [Staphylococcus aureus subsp. aureus NCTC 8325]

ref|YP_001333445.1| **G** transcriptional regulator MarR family protein [Staphylococcus aureus Subsp. aureus str. Newman]

gb|ABD31821.1| **G** conserved hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]

dbj|BAF68683.1| **G** transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]
Length=152

GENE ID: 3921258 SAOUHSC 02819 | hypothetical protein
[Staphylococcus aureus subsp. aureus NCTC 8325]

Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

```
Query 35  LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVL 93
L+ TQ HI+ L+      N K ++E L +S A+TK++KKL ++L+ S      ++R V
Sbjct 34  LSLTQFHIIELIDNNDKVNKKFLSEMLNVSKPAITKSIKKLLAKDLVESHNEFNKREVN 93

Query 94  WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
+SLT+K ++ H HEK++ Y+E+ F D+E VI +FL+ EE +
Sbjct 94  YSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDEMAVIEFLNRSIEELK 145
```

>ref|ZP_03563431.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6008]

ref|ZP_03566444.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6009]
Length=154

Score = 61.2 bits (147), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 65/112 (58%), Gaps = 1/112 (0%)

```
Query 35  LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVL 93
L+ TQ HI+ L+      N K ++E L +S A+TK++KKL ++L+ S      ++R V
Sbjct 36  LSLTQFHIIELIDNNDKVNKKFLSEMLNVSKPAITKSIKKLLAKDLVESHNEFNKREVN 95

Query 94  WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
SLT+K ++ H HEK++ Y+E+ F D+E VI +FL+ EE +
Sbjct 96  CSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDEMAVIEFLNRSIEELK 147
```

>ref|YP_174450.1| **G** MarR family transcriptional regulator [Bacillus clausii KSM-K16]

dbj|BAD63489.1| **G** MarR family transcriptional regulator [Bacillus clausii KSM-K16]
Length=153

GENE ID: 3204362 **ABC0950** | MarR family transcriptional regulator
[Bacillus clausii KSM-K16] (10 or fewer PubMed links)

Score = 60.5 bits (145), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/128 (31%), Positives = 73/128 (57%), Gaps = 3/128 (2%)

```
Query 18  AENKHEILLGKCESDV--KLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKKL 74
A+ + + + G E +      T TQ HI+ ++ EQ + N +AE L +S A+TKA+KKL
Sbjct 21  ADRRRKAMKGSQEESIVSDWTLTQLHIVAIVKEQERANNTMLAEHLNVSKPAITKAVKKL 80

Query 75  QEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVIS 134
+Q++++ ++ +++++ V + LT+      +A H+ HE+ + Y + +F E E I
Sbjct 81  LDQQILEKTQQADNKKEVYYRLTKSGEMLAFIHSQLEHQAARNRYMRIFAEFNSTELETII 140

Query 135  KFLSALTE 142
+FL AL E
Sbjct 141  RFLHALAE 148
```

>ref|YP_080661.1| **G** transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
 gb|AAU25023.1| **G** probable transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
 Length=157

GENE ID: 3028745 yvnA | transcriptional regulator YvnA
 [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

Query 36 TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDEVRVL 93
 T TQ HI+ L++E + NA +A KL+IS AAVTKA+ L + +I+S + N+ + +
 Sbjct 47 TLTQLHIISLISESEADVNNNAFLAAKLQISKAATKAVNVLTKHGMIESHKPPNNNKELY 106
 Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
 ++LT++ +A H HE Y EL ++F++ E + + +FL+
 Sbjct 107 YTLTDEGKKLADIHDMHEIAKQRYIELFDRFSESELQTVIRFLN 151

>ref|YP_254603.1| **G** hypothetical protein pSHaeC05 [Staphylococcus haemolyticus JCSC1435]
 dbj|BAE05997.1| **G** unnamed protein product [Staphylococcus haemolyticus JCSC1435]
 Length=155

GENE ID: 3431756 pSHaeC05 | hypothetical protein
 [Staphylococcus haemolyticus JCSC1435] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 38/119 (31%), Positives = 69/119 (57%), Gaps = 1/119 (0%)

Query 28 KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRAT 86
 K D+ L+ TQ HI+ +++ N K +AE+L +S AVTK++KKL +EL+
 Sbjct 29 KGNEDMDLSLTQFHIEIIDKHEKVNKKFLAEELNVSKPAVTKSIKKLLSKELVVELNNE 88
 Query 87 NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 +++R V ++LT++ ++ H H+K + Y+E+ F ++E E I +FL +E +
 Sbjct 89 SNKREVVYNNLTGRGEKLSFIHDDLHKKAVKKYEEVLKVFDEKEMETIEFLKRSVDELK 147

>ref|YP_093087.1| **G** YvnA [Bacillus licheniformis ATCC 14580]
 gb|AAU42394.1| **G** YvnA [Bacillus licheniformis DSM 13]
 Length=160

GENE ID: 3100261 yvnA | similar to proteins from B. subtilis
 [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

Query 36 TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDEVRVL 93
 T TQ HI+ L++E + NA +A KL+IS AAVTKA+ L + +I+S + N+ + +
 Sbjct 50 TLTQLHIISLISESEADVNNNAFLAAKLQISKAATKAVNVLTKHGMIESHKPPNNNKELY 109
 Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
 ++LT++ +A H HE Y EL ++F++ E + + +FL+
 Sbjct 110 YTLTDEGKKLADIHDMHEIAKQRYIELFDRFSESELQTVIRFLN 154

>ref|ZP_00738634.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
 gb|EA057135.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
 Length=156

Score = 55.8 bits (133), Expect = 9e-07, Method: Compositional matrix adjust.
 Identities = 32/106 (30%), Positives = 64/106 (60%), Gaps = 2/106 (1%)

Query 36 TSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDEVRVL 93
 T TQ HI+ ++E Q N ++ +L IS A ++KA++ L + +++ + + T++++ +
 Sbjct 46 TLTQLHIVSVIHESKQQMNTLLSMELNISKATISKAIRVLIDNKILLTHQNTDNKKEIF 105
 Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSA 139
 ++LT+K + +A H H+ Y EL +F D E +++KFL A
 Sbjct 106 YTLTDKGIQLAIVHKKLHKIAHERYSELFQQFNDSELQIVTKFLEA 151

>ref|ZP_02613091.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
 gb|EDT83321.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
 Length=174

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATN 87
 ++D+K S E H++ + + +S N IA +L ++ ++K KL +++IK+ + N
 Sbjct 58 DNDIKGISLSEFHVIEICIGKNNSNNIFIARELNMTKGGISKINSKLLSKDIIKADKIEN 117
 Query 88 DERVVLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I KFL L
 Sbjct 118 DKREIYSLTEKGIALFKLHEYLHEKEREKLMKILSNYKLEETITLKFLEDL 170

>ref|YP_001253547.1| **G** MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 3502]
 ref|YP_001383390.1| **G** MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 19397]
 ref|YP_001386937.1| **G** MarR family transcriptional regulator [Clostridium botulinum A str. Hall]
 emb|CAL82569.1| **G** MarR-family transcriptional regulator [Clostridium botulinum A str. ATCC 3502]
 gb|ABS35317.1| **G** transcriptional regulator, MarR family [Clostridium botulinum A str. ATCC 19397]
 gb|ABS36227.1| **G** transcriptional regulator, MarR family [Clostridium botulinum A str. Hall]
 Length=174

GENE ID: 5185271 CBO1016 | MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 3502] (10 or fewer PubMed links)
 Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATN 87
 ++D+K S E H++ + + +S N IA++L ++ ++K KL +++IK+ + N
 Sbjct 58 DNDIKGISLSEFHVIEICIGNNMSNNIFIAKELNMTKGGISKINSKLLSKDIKADKIEN 117

Query 88 DERVVLSLSTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I KFL L
 Sbjct 118 DKREIYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTLKFLLEDL 170

>ref|YP_001780642.1| **G** MarR family transcriptional regulator [Clostridium botulinum B1 str. Okra]
 gb|ACA44681.1| **G** transcriptional regulator, MarR family [Clostridium botulinum B1 str. Okra]
 Length=174

GENE ID: 6149223 CLD 3550 | MarR family transcriptional regulator [Clostridium botulinum B1 str. Okra] (10 or fewer PubMed links)
 Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATN 87
 ++D+K S E H++ + + +S N IA++L ++ ++K KL +++IK+ + N
 Sbjct 58 DNDIKGISLSEFHVIEICIGNNMSNNIFIAKELNMTKGGISKINSKLLSKDIKADKIEN 117

Query 88 DERVVLSLSTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I KFL L
 Sbjct 118 DKREIYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTLKFLLEDL 170

>ref|YP_001033131.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 emb|CAL98430.1| **G** transcriptional regulator, MarR family [Lactococcus lactis subsp. cremoris MG1363]
 Length=295

GENE ID: 4797387 rmaB | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)
 Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

Query 42 ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVVLSLSTEKAV 101
 ++ L E TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTEK
 Sbjct 47 LVELWNEDGLTNAEIAELLDIKPSSVTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR 106

Query 102 PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE 142
 + T H T GN TDEEQE ++ + L E
 Sbjct 107 EAQETRDTHNDISETI--FGN-LTDEEQEQLANLMEKLVE 144

>ref|ZP_02617530.1| transcriptional regulator, MarR family [Clostridium botulinum Bf]
 gb|EDT85893.1| transcriptional regulator, MarR family [Clostridium botulinum Bf]
 Length=174

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATN 87
 ++D+K S E H++ + + +S N IA+ L ++ ++K KL +++IK+ + N
 Sbjct 58 DNDIKGISLSEFHVIEICIGNNMSNNIFIAKDLNMTKGGISKINSKLLSKDIKADKIEN 117

Query 88 DERVVLSLSTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I KFL L
 Sbjct 118 DKREIYSLTEKGIALFKLHEHIHEKEREKLMKILSNYKLEEITTLKFLLEDL 170

>ref|YP_861960.1| **G** MarR family transcriptional regulator [Gramella forsetii KT0803]
 emb|CAL66893.1| **G** MarR family transcriptional regulator protein [Gramella forsetii

KT0803]
Length=158

GENE ID: 4650237 GFO 1928 | MarR family transcriptional regulator
[Gramella forsetii KT0803] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 65/112 (58%), Gaps = 8/112 (7%)

```
Query 1  MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQ--ISTNAKIAE 58
          + L NQI  + ++ +  ++ L K E  LT Q  +L++L E+  +S N KI E
Sbjct 7  LKLENQICFPIYSVSRILITKAYKPYLDKLE---LTPQYLVLLVWEEHKLSVN-KIGE 61

Query 59  KLIKSPAAVTKALKKLEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH 110
          KL ++  ++ LK++++ EL+K +R++NDER VL LT+K +  KE A H
Sbjct 62  KLMLNTNTLSPLLKRMEKNELLKRNSSNDERTVLVGLTDKGLSY-KEKAAH 112
```

>ref|NP_391388.1| **G** hypothetical protein BSU35080 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03593305.1| hypothetical protein Bsubs1_18986 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03597590.1| hypothetical protein BsubsN3_18902 [Bacillus subtilis subsp. subtilis str. NCIB 3610]
6 more sequence titles

ref|ZP_03601994.1| hypothetical protein BsubsJ_18865 [Bacillus subtilis subsp. subtilis str. JH642]
ref|ZP_03606279.1| hypothetical protein BsubsS_19021 [Bacillus subtilis subsp. subtilis str. SMY]
sp|P40762.1|YVMB_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator yvmb
emb|CAA85355.1| unnamed protein product [Bacillus subtilis]
gb|AAC67278.1| YzhA [Bacillus subtilis]
emb|CAB15513.1| **G** yvmb [Bacillus subtilis subsp. subtilis str. 168]
Length=169

GENE ID: 936625 yvmb | yvmb [Bacillus subtilis subsp. subtilis str. 168]
(10 or fewer PubMed links)

Score = 53.5 bits (127), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 36/91 (39%), Positives = 53/91 (58%), Gaps = 2/91 (2%)

```
Query 52  TNAKIAEKLKISPAAVTKALKKLEQELIKSSRATNDERVVLWSLTEKAVPVAKEH-ATH 110
          NA IA K+ +S A VTK KL ++E I S + T++++ V + LT K + H H
Sbjct 63  NNAGIARKMNLKANVTIKISTKLIKEEFINSYQLTDNKKEVYFKLTRKGRIFDLHEKLH 122

Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
          +K L+ YQ L + F+ EEQ+ + KFL LT
Sbjct 123 KKKELAFYQFL-DSFSQEEQKAVLKFLQLT 152
```

>ref|ZP_02994615.1| hypothetical protein CLOSP0_01734 [Clostridium sporogenes ATCC 15579]
gb|EDU38872.1| hypothetical protein CLOSP0_01734 [Clostridium sporogenes ATCC 15579]
Length=174

Score = 53.5 bits (127), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 34/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

```
Query 30  ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLEQELIKSSRATN 87
          ++D+K S E H++ + + +S N IA++L ++ ++K KL +++IK+ + N
Sbjct 58  DNDIKEISLSEFHVIEICIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIKADKIEN 117

Query 88  DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
          D+R + +SLTEK + + K H H+K ++ + + EE I KFL L
Sbjct 118 DKREIYYSLTEKGIVLFLKHEYLHKKEQEKLMLKILSNYKQEEITILKFLDDL 170
```

>ref|ZP_01994138.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
gb|EDM64274.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
Length=153

Score = 53.1 bits (126), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 55/111 (49%), Gaps = 4/111 (3%)

```
Query 35  LTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLEQELIKSSRATNDERVVL 93
          LT+ H++ + N + IA KL I+ ++T A+ L + ++ R+ D RVVL
Sbjct 37  LTNNDMHVIEAVGLGDGNMSSIAKRLNITVGLSTTAMNSLVNKRYVERHRSEEDRRVVL 96

Query 94  WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
          LTEK V H +H + Q + +K D E V+ K L AL+E F
Sbjct 97  VKLTEKGVKAYHHHEDYHRQMT---QAILDKLDDTELPVLVKTLDALSEFF 144
```

>ref|ZP_03294064.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM 13275]
gb|EEA84316.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM 13275]
Length=166

Score = 53.1 bits (126), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 37/131 (28%), Positives = 68/131 (51%), Gaps = 6/131 (4%)

```
Query 13  TIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKAL 71
```

Sbjct 20 T +F HE G+ K+ + H++ + E N +++E+L I+ AV++ L
 TYYKFLSTPHEYPGE-----KMHMREHVHTEIGEGGLDNISELSERLNITKGAVSQYL 74

Query 72 KKLQEQELIKSSRATNDEVRVLSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
 KKL+++ I+ + + D+R LTK + K H + E+ + N+FT+EE E

Sbjct 75 KKLEKKGFIERVQESDKRQYSVRLTEKGKELDKIHTKYDEEQYAKACFFNFETEELE 134

Query 132 VISKFLSALTE 142
 +I +F + E

Sbjct 135 LICRFEARFAE 145

>ref|ZP_02211326.1| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
 gb|EDQ97187.1| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
 Length=150



Score = 52.4 bits (124), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 33/94 (35%), Positives = 50/94 (53%), Gaps = 3/94 (3%)

Query 52 TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDEVRVLSLTKAVPVAKEHATHH 111
 T +IA L+I+ +T A+ +L ++ + SR D RVVL SLTEK K HA H

Sbjct 53 TMGEIAHDLRITVGTLSAINRLIKGYAERSRTEEDRRRVVLSLTKGKHAYKIHADFH 112

Query 112 EKTLSYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 ++ + Q N + DEEQEV+ + + F+

Sbjct 113 KEMV---QATLNSYNDEEQEVLCDVIEKINIFFE 143

>ref|YP_001390364.1|  MarR family transcriptional regulator [Clostridium botulinum F str. Langeland]
 gb|ABS39442.1|  transcriptional regulator, MarR family [Clostridium botulinum F str. Langeland]
 Length=174

GENE ID: 5405444 CLI 1098 | MarR family transcriptional regulator
 [Clostridium botulinum F str. Langeland]



Score = 52.4 bits (124), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 34/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN 87
 ++D+K S E H++ + + +S N IA++L ++ ++K KL +++IK+ + N

Sbjct 58 DNDIKGISLSEFHVIEICIGNNMSNNIFIAKELNMTRGGISKINSKLLSKDIKADKIEN 117

Query 88 DERVVLSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I FL L

Sbjct 118 DKREIYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITILNFLEDL 170

>ref|YP_001786407.1|  MarR family transcriptional regulator [Clostridium botulinum A3 str. Loch Maree]
 gb|ACA55750.1|  transcriptional regulator, MarR family [Clostridium botulinum A3 str. Loch Maree]
 Length=174

GENE ID: 6154364 CLK 0459 | MarR family transcriptional regulator
 [Clostridium botulinum A3 str. Loch Maree] (10 or fewer PubMed links)


Score = 51.6 bits (122), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 33/113 (29%), Positives = 62/113 (54%), Gaps = 2/113 (1%)


Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN 87
 ++D+K S E H++ + + +S N IA++L ++ ++K KL +++I++ + N

Sbjct 58 DNDIKGISLSEFHVIEICIGNNPNPNIFIAKELNMTRGGISKINSKLLKDIIRADKIEN 117

Query 88 DERVVLSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I KFL L

Sbjct 118 DKREIYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKQEEITILKFLEDL 170

>ref|YP_808725.1|  transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]

gb|ABJ72303.1|  Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=292

GENE ID: 4432217 LACR 0742 | transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

Query 52 TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDEVRVLSLTKAVPVAKEHATHH 111
 TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTK + T H

Sbjct 57 TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTH 116

Query 112 EKTLSYQELGNKFTDEEQEVISKFLSALTE 142
 T GN TDEEQ+ ++ + L E

Sbjct 117 NDISETI--FGN-LTDEEQQLANLMEKLVE 144

>ref|YP_001698248.1| **G** MarR family transcriptional regulator [Lysinibacillus sphaericus C3-41]

gb|ACA40118.1| **G** transcriptional regulator, MarR family [Lysinibacillus sphaericus C3-41]
Length=162

GENE ID: 6022244 Bsph 2567 | MarR family transcriptional regulator [Lysinibacillus sphaericus C3-41] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

```
Query 36  TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLW 94
           T TQ HI+ + Q S N ++E L +S A+TKA+KK+ E+ +I +R +++ V +
Sbjct 44  TLTQLHIVSAIKAQGSANNTFLSETLNVSKPAITKAIKKMLEKNVIVETRQEANQKEVHY 103

Query 95  SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
           LT ++ H HEK + Y L + F +E E I FL +T++ +
Sbjct 104 LLTAFGKQLSSIHEQLHEKARNRYRLRLDSFNTDELETIVTFLEMITDKLK 154
```

>ref|NP_266864.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]

gb|AAK04806.1|AE006304_6 **G** transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=291

GENE ID: 1114333 rnaB | transcription regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query 52  TNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH 111
           TNA+IAE L I P++VT +K+L+E E++ + ND+RV LT+K + T H
Sbjct 57  TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTHM 116

Query 112 EKTLSYQELGNKFTDEEQEVISKFLSALTE 142
           T GN TDEEQE ++ + L E
Sbjct 117 NDISETI--FGN-LTDEEQEQLAFLMEKLVE 144
```

>ref|ZP_01723095.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]

gb|EAZ86562.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
Length=162

Score = 50.4 bits (119), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 35/111 (31%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

```
Query 36  TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLW 94
           T TQ HI+ + Q S N ++E L +S A+TKA+KK+ E+ +I +R +++ + +
Sbjct 44  TLTQLHIVSAIKAQGSANNTFLSETLNVSKPAITKAIKKMLEKNVIVETRQEANQKEIHY 103

Query 95  SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
           LT ++ H HEK + Y L + F +E E I FL +T++ +
Sbjct 104 LLTAFGKQLSSIHEQLHEKARNRYRLRLDSFNTDELETITITFLEMITDKLK 154
```

>ref|YP_808147.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]

gb|ABJ71725.1| **G** Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=169

GENE ID: 4432499 LACR 0099 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 50.4 bits (119), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query 41  HILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKA 100
           HIL L ++ T ++A KL ++ VT+A++ L + + + + +A ND++ + + +T K
Sbjct 53  HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKQFLTTYQADNDKKKIYYHITTKG 112

Query 101 VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
           + VA H H+ ++ +K+ + E+ +I FLS
Sbjct 113 LKVASIHDKMHKIMDLKLGQIFDKYNEKSIILNFLS 150
```

>ref|NP_786298.1| **G** transcription regulator [Lactobacillus plantarum WCFS1]

emb|CAD65154.1| **G** transcription regulator [Lactobacillus plantarum WCFS1]
Length=178

GENE ID: 1063436 lp_2967 | transcription regulator [Lactobacillus plantarum WCFS1] (10 or fewer PubMed links)

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 33/104 (31%), Positives = 57/104 (54%), Gaps = 5/104 (4%)

```
Query 39  QEHLMLLAEQIS--TNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSL 96
           Q IL +LA+ + TNA+IAE L I P++V+ L +L++ LI+ + +D+RVV+ L
Sbjct 43  QMGILRVLADAPAGLTNAEIAEILDIPSSVSATLNRLLEDGGLIEREPSAHDKRVVIVRL 102
```

Query 97 TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 +++ +A A + T +L TD+E+ + L L
 Sbjct 103 SDRGREMADHRA---QGTSDLADQLFGNLTDDERNQLQHLLDKL 143

>ref|YP_757477.1| **G** MarR family transcriptional regulator [Maricaulis maris MCS10]
 gb|ABI66539.1| **G** transcriptional regulator, MarR family [Maricaulis maris MCS10]
 Length=143

GENE ID: 4285355 Mmar10_2247 | MarR family transcriptional regulator
 [Maricaulis maris MCS10]

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 39/146 (26%), Positives = 75/146 (51%), Gaps = 5/146 (3%)

Query 1 MSLANQIDQLGTIMQFAENK-HEILLGKCESDVKLTSTQEHILMLLAEQISTN-AKIAE 58
 M+ A +D+ L +++ A K + + +S +TS Q +L LLA + I E
 Sbjct 1 MARARAVDRRLFLLEIAARKLNRDADARLKSVAQAVLFLARRGERRMGDIGE 60
 Query 59 KLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTY 118
 L + P AVT + +++ L+ + +D+R + SLTEK + + A H + L+T
 Sbjct 61 MLSLHPPAVTGLVNRMEALGLVTKKTSKPSDKRSAIVSLTEKGRALG-DTADHILRDLNT- 118
 Query 119 QELGNKFTDEEQEVISKFLSALTEEF 144
 EL N+ +E+ +++ + L+ + +F
 Sbjct 119 -ELENRLGEEDADMLHRVLTRIAVDF 143

>ref|NP_391385.1| **G** hypothetical protein BSU35050 [Bacillus subtilis subsp. subtilis str. 168]
 ref|ZP_03593302.1| hypothetical protein Bsubs1_18971 [Bacillus subtilis subsp. subtilis str. 168]
 ref|ZP_03597587.1| hypothetical protein BsubsN3_18887 [Bacillus subtilis subsp. subtilis str. NCIB 3610]
 ref|ZP_03601991.1| hypothetical protein BsubsJ_18850 [Bacillus subtilis subsp. subtilis str. JH642]
 ref|ZP_03606276.1| hypothetical protein BsubsS_19006 [Bacillus subtilis subsp. subtilis str. SMY]
 sp|O34692.1|YVNA_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator yvna
 gb|AAC67281.1| Yvna [Bacillus subtilis]
 emb|CAB15510.1| **G** yvna [Bacillus subtilis subsp. subtilis str. 168]
 Length=157

GENE ID: 936639 yvna | yvna [Bacillus subtilis subsp. subtilis str. 168]
 (10 or fewer PubMed links)

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 30/104 (28%), Positives = 59/104 (56%), Gaps = 1/104 (0%)

Query 36 TSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW 94
 T TQ HI+ + Q N+ +A +L IS AAV+KA+ L + +I ++ +++ + +
 Sbjct 48 TLTQLHIVSCIHTSQNVNNSFLASRLHISKAASVAVHALLKHNIITVTKKPGNKKEIFY 107
 Query 95 SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
 +LT+ +A H HEK Y++L N+F+ ++ + ++ F +
 Sbjct 108 TLTDGRKLAALHEQLHEKAKEQYKQLFNEFSIDDLKTVTAFFN 151

>ref|NP_111681.1| **G** transcription regulator (SlyA-related) [Thermoplasma volcanium GSS1]
 dbj|BAB60329.1| **G** hypothetical protein [Thermoplasma volcanium GSS1]
 Length=143

GENE ID: 1441302 TVN1162 | transcription regulator (SlyA-related)
 [Thermoplasma volcanium GSS1] (10 or fewer PubMed links)

Score = 49.7 bits (117), Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 30/81 (37%), Positives = 45/81 (55%), Gaps = 0/81 (0%)

Query 26 LGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA 85
 +G+ S + + IL LL+E ST K+AE ++PA +T L +++ Q LI SR+
 Sbjct 27 MGESLSHISAKPIEVRIYLLSEDESTVNKLAELTDVTPAWITGTLDEMESQGLIVRSRS 86
 Query 86 TNDERVVLWSLTEKAVPVAKE 106
 D RVV +TEK + V E
 Sbjct 87 GEDRRVVNVHITEKGIEVLNE 107

>ref|NP_419215.1| **G** MarR family transcriptional regulator [Caulobacter crescentus CB15]
 ref|YP_002515775.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus NA1000]
 gb|AAK22383.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus CB15]
 gb|ACL93867.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus NA1000]
 Length=147

GENE ID: 942105 CC_0396 | MarR family transcriptional regulator
 [Caulobacter crescentus CB15] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 32/119 (26%), Positives = 63/119 (52%), Gaps = 4/119 (3%)

```
Query 27 GKCESDVKLTSTQEHILMLLAEQIST-NAKIAEKLKISPAAVTKALKKKLQEQELIKSSRA 85
          G+ ++ LT+ Q +L L E+ + A+ L ++P+A+T + ++ EL++
Sbjct 26 GRMAAEGGLTAAQSGVLFFLGERDGLIGEADALDLPASMTGLIDRMARAE LVERRAD 85

Query 86 TNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
          D R + LT+K A++ A + ++ +L FTDEE V+S++L++L +F
Sbjct 86 AKDGRAMHLHLTDKGR-AARDTAKAGLRGVNA--QLTEGFTDEEISVVSRLASLQTKF 141
```

>ref|YP_001031482.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MGL363]

emb|CAL96727.1| **G** transcriptional regulator, MarR family [Lactococcus lactis subsp. cremoris MGL363]
Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MGL363] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query 41 HILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKA 100
          HIL L ++ T ++A KL ++ VT+A++ L + + + + +A ND++ + + +T K
Sbjct 56 HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTYYQADNDKKKIYYHITKG 115

Query 101 VPVAKHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
          + VA H H+ ++ +K+ + ++ +I FLS
Sbjct 116 LKVASIHDKMHKIMDKLKGQIFDKYNENDKSIILNLS 153
```

>ref|NP_603578.1| **G** MarR family transcriptional regulator [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]

gb|AAL94877.1| **G** Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
Length=225

GENE ID: 991648 FN0681 | MarR family transcriptional regulator
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

```
Query 35 LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVV 92
          LT T+ HI+ + E Q++ N ++A+K+ I+ T A+ KL ++ I +R+T D R V
Sbjct 34 LTHTELHIIESIGENTQLTMN-ELADKIGITMGATVAISKLSDKGYIDRARSTTDRRKV 92

Query 93 LWSLTEKAVPVAKEHATHHEKTLSTYQE 120
          SLT+K V H +H+ +++ E
Sbjct 93 FVSLTKKGVDAITYHNNYHKMIMASITE 120
```

>ref|YP_138915.1| **G** MarR family transcriptional regulator [Streptococcus thermophilus LMG 18311]

gb|AAV60100.1| **G** transcriptional regulator, MarR family [Streptococcus thermophilus LMG 18311]
Length=144

GENE ID: 3164787 stu0381 | MarR family transcriptional regulator
[Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

```
Query 51 STNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH 110
          +T + +A +L ++ VT +L KL+++ I +R++ D RVV SL++K V + H
Sbjct 50 TTPSAVARELMLTLGTVTTSNLKLEKKGYYIRTRSSVDRRVVHLSLSKKGRILVYRLHRGF 109

Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
          H+ + T E F DEE +V+SK L L
Sbjct 110 HKSMVKTITE---GFNDEELKVMKGLLENL 136
```

>ref|YP_002165566.1| **G** possible MarR family transcriptional regulator [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

gb|EDK89119.1| **G** possible MarR family transcriptional regulator [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]
Length=225

GENE ID: 6818656 FNP_1336 | possible MarR family transcriptional regulator
[Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

```
Query 35 LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVV 92
          LT T+ HI+ + E Q++ N ++A+K+ I+ T A+ KL ++ I +R+T D R V
Sbjct 34 LTHTELHIIESIGENTQLTMN-ELADKIGITMGATVAISKLSDKGYIDRARSTTDRRKV 92

Query 93 LWSLTEKAVPVAKEHATHHEKTLSTYQE 120
          SLT+K V H +H+ +++ E
```

Sbjct 93 FVSLTKKGVDALTYHNNYHKMIMASITE 120

>ref|ZP_00144611.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. Vincentii ATCC 49256]
 gb|EAA23791.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
 Length=225

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query 35 LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE RVV 92
 LT T+ HI+ + E Q++ N ++A+K+ I+ T A+ KL ++ I +R+T D R V
 Sbjct 34 LTHTELHIIESIGENTQLTMN-ELADKIGITMGATVAISKLSDKGYIDRARSTDRRKV 92
 Query 93 LWSLTEKAVPVAKEHATHHEKTLSTYQE 120
 SLT+K V H +H+ +++ E
 Sbjct 93 FVSLTKKGVDALTYHNNYHKMIMASITE 120

>ref|YP_819912.1| **G** MarR family transcriptional regulator [Streptococcus thermophilus LMD-9]

gb|ABJ65716.1| **G** transcriptional regulator, MarR family [Streptococcus thermophilus LMD-9]
 Length=144

GENE ID: 4437359 STER 0428 | MarR family transcriptional regulator
 [Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

Query 51 STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE RVV LWSLTEKAVPVAKEHATH 110
 +T + +A +L ++ VT +L KL+++ I +R++ D RVV SL++K V + H
 Sbjct 50 TTPSAVARELMLTLGTVTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRAF 109
 Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 H+ + T E F DEE +V+SK L L
 Sbjct 110 HKSMVKTITE---GFNDEELKVMKSGLENL 136

>ref|YP_079349.1| **G** transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]

gb|AAU23711.1| **G** possible transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]
 Length=161

GENE ID: 3031484 yvmB | transcriptional regulator YvmB
 [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 48.5 bits (114), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

Query 29 CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR 84
 ESDVK T H++ + ++ N IA+K+ +S A +TK KL ++ LIK +
 Sbjct 36 AESDVKRLPGNMTTIHVISCIGHDEPINNTGIAKKMNLKANITKISSKLLKEGLIKRFQ 95
 Query 85 ATNDE RVV LWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
 T++++ + + LT V + H H++ + + F+ EQ I KFL LT
 Sbjct 96 LTDNKKIEIYFRLTPSGKQVFELHEKLHQKADQFSRFLDSFSTAEQGAILKFLQGLT 152

>ref|ZP_01219563.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]

gb|EAS43796.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]
 Length=138

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

Query 7 IDQFLGTIMQFAEN----KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK 61
 I+Q TI++F E + ++ GK + Q HI+ +L + K +A+K+
 Sbjct 4 IEQLNHTIIEFYEKLSWEQSVVRGKG-----FSLPQVHIVEILGAHGAMRMKELADKIG 58
 Query 62 ISPAAVTKALKKLQEQELIKSSRATNDE RVV LWSLTEKAVPVAKEHATHHEKTLSTYQEL 121
 ++ +T + K+ + ELI+ +D R +L L TEK V + +EH H LS Q++
 Sbjct 59 VTTGTLTVQVDKMQAELIQRPHESDRRSILVDLTEKGVEMYQEHDHLH---LSLTQDI 115
 Query 122 GNKFTDEEQEVISKFLSALTEEF 144
 + D E++ + +L+ + +EF
 Sbjct 116 TAQLDDVERKNLLMYLTKMNQEF 138

>ref|YP_091766.1| **G** YvmB [Bacillus licheniformis ATCC 14580]


gb|AAU41073.1| **G** YvmB [Bacillus licheniformis DSM 13]
 Length=163


GENE ID: 3097946 yvmB | YvmB [Bacillus licheniformis ATCC 14580]
 (10 or fewer PubMed links)

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

Query 29 CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSR 84
 ESDVK T H++ + ++ N IA+K+ +S A +TK KL ++ LIK +
 Sbjct 38 AESDVKRLPGNMTTIHVISCIGHDEPINNTGIAKKNLSKANITKISSKLLKEGLIKRFQ 97

Query 85 ATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
 T++++ + + LT V + H H++ + + F+ EQ I KFL LT
 Sbjct 98 LTDNKKIYFRLTPSGKQVFELHEKLHQKADQFSRFLDSFSTAEQGAILKFLQGLT 154

>ref|YP_129221.1|  MarR family transcriptional regulator [Photobacterium profundum SS9]

emb|CAG19419.1|  putative transcriptional regulator, MarR family [Photobacterium profundum SS9]
 Length=138

GENE ID: 3122954 PBPR1008 | MarR family transcriptional regulator
 [Photobacterium profundum SS9] (10 or fewer PubMed links)

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

Query 7 IDQFLGTIMQFAEN---KHEILLGKCESDVKLSTQEHILMLLAEQISTNAK-IAEKLK 61
 I+Q TI++F E + ++ GK + Q HI+ +L + K +A+K+
 Sbjct 4 IEQLNHTIIEFYEKLSSWEQSVVRGK-----FSLPQIHIVEILGAHGAMRMKELADKIG 58

Query 62 ISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL 121
 ++ +T + K+ + ELI+ +D R +L LTE+ V + +EH H LS Q++
 Sbjct 59 VTTGTLTVQVDKMQAELIQRRPHESDRRSILVDLTEQGVEMYQEHDLH---LSLTQDI 115

Query 122 GNKFTDEEQEVISKFLSALTEEF 144
 K D E++ + +L+ + +EF
 Sbjct 116 TAKLDDTERKNLLMYLTKMNQEF 138


>ref|ZP_00990845.1| hypothetical transcriptional regulator, MarR family [Vibrio splendidus 12B01]


gb|EAP94213.1| hypothetical transcriptional regulator, MarR family [Vibrio splendidus 12B01]
 Length=301

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 62/117 (52%), Gaps = 1/117 (0%)

Query 25 LLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSR 84
 +L K D+ L Q H L+ L +Q T ++A+KL I + ++A+ L + LI++S
 Sbjct 19 MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP 78

Query 85 ATNDERVVLWSLTEKAV-PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 ND+R V+ S+TE+ + +A+ H+ ++ S + L T + I +L AL
 Sbjct 79 HPNDKRSVVASVTEQGIKTLAQLHSQQNQFYDSVLERLLEAETQQVSGGIKHYLKAL 135

>ref|YP_001319891.1|  MarR family transcriptional regulator [Alkaliphilus metalliredigens QYMF]


gb|ABR48232.1|  transcriptional regulator, MarR family [Alkaliphilus metalliredigens QYMF]
 Length=143


GENE ID: 5312143 Amet 2072 | MarR family transcriptional regulator
 [Alkaliphilus metalliredigens QYMF]

Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 42/67 (62%), Gaps = 1/67 (1%)

Query 35 LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVL 93
 +T TQ L++L E+ AK + EKL + +T LKKL+ +ELI R+T DER+++
 Sbjct 37 ITYTQYITLLVLWEKPKITAKELGEKLYLDSGTLTPLLKKLESKELITRKRSTKDERIMI 96

Query 94 WSLTEKA 100
 +LT+K
 Sbjct 97 VLTLDKG 103

>ref|YP_001838202.1|  MarR family transcriptional regulator [Leptospira biflexa serovar Patoc sStrain 'Patoc 1 (Paris)']

gb|ABZ96926.1|  Putative transcriptional regulator, MarR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']
 Length=133

GENE ID: 6222463 LEPBI I0798 | MarR family transcriptional regulator
 [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']
 (10 or fewer PubMed links)

Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)





Query 31 SDVKLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDE 89
 +D+ LT Q +++++ E+ IST +KI +KL++ +T LK+L++ EL+ R NDE
 Sbjct 26 ADLGLTPQYLVMLVMWEEKISTVSKIGDKLQLDSGTLTPLLKRLEQMELLDRMRNPND 85

Query 90 RVLWSLTEKA 100
 R V L++K
 Sbjct 86 RSVNIVLSKKG 96

>ref|YP_108512.1| **G** putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]
 ref|YP_102754.1| **G** MarR family transcriptional regulator [Burkholderia mallei ATCC 23344]
 ref|ZP_00438156.1| COG1846: Transcriptional regulators [Burkholderia mallei GB8 horse 4]
 46 more sequence titles

ref|YP_333321.1| **G** MarR family transcriptional regulator [Burkholderia pseudomallei 1710b]
 ref|YP_992831.1| **G** MarR family transcriptional regulator [Burkholderia mallei SAVP1]
 ref|YP_001026174.1| **G** MarR family transcriptional regulator [Burkholderia mallei NCTC 10229]
 ref|YP_001058785.1| **G** MarR family transcriptional regulator [Burkholderia pseudomallei 668]
 ref|YP_001080556.1| **G** MarR family transcriptional regulator [Burkholderia mallei NCTC 10247]
 ref|YP_001066038.1| **G** MarR family transcriptional regulator [Burkholderia pseudomallei 1106a]
 ref|ZP_01769009.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
 ref|ZP_02102319.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1106b]
 ref|ZP_02109049.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1710a]
 ref|ZP_02266811.1| transcriptional regulator, MarR family protein [Burkholderia mallei PRL-20]
 ref|ZP_02403045.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei DM98]
 ref|ZP_02411585.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 14]
 ref|ZP_02447714.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 91]
 ref|ZP_02455880.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 9]
 ref|ZP_02471448.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei B7210]
 ref|ZP_02481920.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 7894]
 ref|ZP_02490126.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei NCTC 13177]
 ref|ZP_02498250.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 112]
 ref|ZP_02506273.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei BCC215]
 ref|YP_002009903.1| **G** transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
 ref|YP_002036065.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
 ref|YP_002022669.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
 ref|YP_002050288.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
 ref|YP_002060819.1| **G** transcriptional regulator, MarR family [Burkholderia mallei FMH]
 ref|YP_002064980.1| **G** transcriptional regulator, MarR family [Burkholderia mallei JHU]
 ref|YP_002106328.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei 406e]
 ref|YP_002110157.1| **G** transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
 ref|ZP_03454874.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
 emb|CAH35912.1| **G** putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]
 gb|AAU48847.1| **G** transcriptional regulator, MarR family [Burkholderia mallei ATCC 23344]
 gb|ABA50381.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei 1710b]
 gb|ABM52457.1| **G** transcriptional regulator, MarR family [Burkholderia mallei SAVP1]
 gb|ABN02741.1| **G** transcriptional regulator, MarR family [Burkholderia mallei NCTC 10229]
 gb|ABN82036.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei 668]
 gb|ABN89050.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei 1106a]
 gb|ABO05799.1| **G** transcriptional regulator, MarR family [Burkholderia mallei NCTC 10247]
 gb|ERA46431.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
 gb|EDK56373.1| **G** transcriptional regulator, MarR family [Burkholderia mallei FMH]
 gb|EDK60534.1| **G** transcriptional regulator, MarR family [Burkholderia mallei JHU]
 gb|EDK85546.1| **G** transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
 gb|EDO84870.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei



406e)

gb|EDO91962.1|  transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
 gb|EDP89187.1|  transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
 gb|EDS86631.1|  transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
 gb|EDU07559.1|  transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
 gb|EEC33252.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
 Length=165

GENE ID: 3092472 BPSL1912 | putative transcriptional regulatory protein [Burkholderia pseudomallei K96243] (10 or fewer PubMed links)

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 33/126 (26%), Positives = 69/126 (54%), Gaps = 5/126 (3%)



Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS 63
 Sbjct 17 QINDSVGYLMRSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSAAELAREYGID 76
 Query 64 PAAVTKALKKLQEQELIKSSSRATNDERVVLWSLTKAVPVAKEHATHHEKTLSTYQELGN 123
 Sbjct 77 ASAITRLLDLDRVEKRGLLQVRSSDDRVRVLELTDEGRALTKRMPAIFRSVL---DEVLD 133
 Query 124 KFTDEE 129
 FT EE
 Sbjct 134 GFTPEE 139

>ref|YP_001961880.1|  Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc sTrain 'Patoc 1 (Ames)']
 gb|ABZ93302.1|  Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
 Length=145

GENE ID: 6388419 LBF_0770 | Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
 (10 or fewer PubMed links)

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

Query 31 SDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSSRATNDE 89
 +D+ LT Q +++++ E+IST +KI +KL++ +T LK+L++ EL+ R NDE
 Sbjct 38 ADLGLTYPQYLVMLVMWEEKISTVSKIGDKLQLDSGTLTPLLKRLEQMELLDRMRNPND 97
 Query 90 RVVLSLTKA 100
 R V L++K
 Sbjct 98 RSVNIVLSKKG 108

>ref|YP_001310724.1|  MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]
 gb|ABR35768.1|  transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
 Length=155

GENE ID: 5294814 Cbei_3649 | MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 30/109 (27%), Positives = 57/109 (52%), Gaps = 1/109 (0%)

Query 34 KLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSSRATNDERV 92
 KLT +Q H + + N K++++L ++ A+TK KKL + + + + + V
 Sbjct 28 KLTFSQIHCAIAIEYIEDANITKLSQELGMTTGAITKMCKKLLNEGYVSKYQKEGNNKEV 87
 Query 93 LWSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
 + LTE + V + H HEK+ + +++ ++ DEE+ I KFL +
 Sbjct 88 YYDLTELGLNVCEIHNRIHEKSYNKKKDIIAQYNDEEKATILKFLHDMN 136

>ref|ZP_01065868.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
 gb|EAQ52745.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
 Length=301

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 26/77 (33%), Positives = 45/77 (58%), Gaps = 0/77 (0%)

Query 25 LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR 84
 +L K D+ L Q H L+ L +Q T ++A+KL I + ++A+ L + LI++S
 Sbjct 19 MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP 78
 Query 85 ATNDERVVLWSLTKAV 101
 ND+R V+ S+TE+ +
 Sbjct 79 HPNDKRSVVASVTEQGI 95

>ref|YP_140799.1| **G** MarR family transcriptional regulator [Streptococcus thermophilus CNRZ1066]

gb|AAV61984.1| **G** transcriptional regulator, MarR family [Streptococcus thermophilus CNRZ1066]
Length=144

GENE ID: 3167129 str0381 | MarR family transcriptional regulator
[Streptococcus thermophilus CNRZ1066] (10 or fewer PubMed links)

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 30/90 (33%), Positives = 50/90 (55%), Gaps = 3/90 (3%)

```
Query 51 STNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH 110
      +T + +A +L ++ VT +L KL+++ I +R++ D RVV SL++K V + H
Sbjct 50 TTPSAVARELMLTLGTVTTSLNKLEKKGYYIIRTRSSVDRRVVHLSLKKGRLVYRLHRGF 109

Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
      H+ S + F DEE +V+SK L L
Sbjct 110 HK---SMVMRITEGFNDEELKVMKGLENL 136
```

>ref|YP_143999.1| **G** MarR family transcriptional regulator [Thermus thermophilus HB8]
dbj|BAD70556.1| **G** transcriptional regulator MarR family [Thermus thermophilus HB8]
Length=144

GENE ID: 3168756 TTHA0733 | MarR family transcriptional regulator
[Thermus thermophilus HB8]

Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 34/109 (31%), Positives = 55/109 (50%), Gaps = 5/109 (4%)

```
Query 35 LTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLW 94
      L+ + H+L LLA+ + +++AE L++ P+ V+ L L+E+ L+K S D R V
Sbjct 36 LSPRKAHLGLLAKGVDLPSQLAELELVHPSQVSHLLAALEEEGLVKRSPDPQDRRKVKL 95

Query 95 SLTEKAVPVAKEHATHHEKT-LSTYQELGNKFTDEEQEVISKFLSALTE 142
      LT P +E A E L+ + + + EEQ + L LTE
Sbjct 96 FLT----PKGREAARTEALWLAVFGRRRLARLSPEEQAAFLRILRKLTE 140
```

>ref|YP_293371.1| **G** regulatory protein, MarR [Ralstonia eutropha JMP134]

gb|AAZ65514.1| **G** regulatory protein, MarR [Ralstonia eutropha JMP134]
Length=150

GENE ID: 3607869 Reut_C6203 | regulatory protein, MarR
[Ralstonia eutropha JMP134]

Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 32/112 (28%), Positives = 58/112 (51%), Gaps = 1/112 (0%)

```
Query 6 QIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHILMLLAEQISTNA-KIAEKLKISP 64
      +I Q +G + A N + + D+ +T Q IL+ L + ++T ++++ L I
Sbjct 15 RITQSVGFLLNRARNLTLLMEMDAALKDLDTGQQMGILLSLTQGVATTFEELSKVLGIDT 74

Query 65 AAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL 116
      +T+ L KL+ + L+ SR+ +D RVV +LT+K VA+ K L+
Sbjct 75 GLMTRMLDKLETKGLLSRSRSLDDRRVNLTLTQKGQVEAERAPVVAPKVLN 126
```

>ref|YP_001307422.1| **G** MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]

gb|ABR32466.1| **G** transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
Length=153

GENE ID: 5291510 Cbei_0278 | MarR family transcriptional regulator
[Clostridium beijerinckii NCIMB 8052]

Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 30/114 (26%), Positives = 62/114 (54%), Gaps = 1/114 (0%)

```
Query 32 DVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDER 90
      D+ L ++ H++ + + NA I+++L ++ A++K KL ++ELIK + N+++
Sbjct 40 DMGLMLSEIHVIDCIGKNQLINATFISKELNMTKGAIKITSKLLKKELIKGNHLENNKK 99

Query 91 VVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
      + ++LT + V K H H+ + ++ +K+ EE +I+ FL L E
Sbjct 100 EIYYTLTAQGKEVFKVHEILHKIESEKFKILSKYDKEELSIINSFLEDLISEL 153
```

>ref|ZP_02950515.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]

gb|EDT74473.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]
Length=145

Score = 46.2 bits (108), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 32/86 (37%), Positives = 48/86 (55%), Gaps = 2/86 (2%)

```
Query 17 FAENKHEILLGK-CESDVKLSTQE-HILMLLAEQISTNAKIAEKLKISPAAVTKALKKKL 74
      +A ++ I L K C LT TQ +L+L ++ ST +I ++L + +T LKK+
Sbjct 19 YAASREVIKLYKPCLDKFNLTYYQVAMLVLWEDEKSTVKEIGKRLHLDSGTLTPLLKKM 78
```


Query 75 QEQELIKSSRATNDERVVLSLTEKA 100
 + ELIK R ND+RVV+ L EK
 Sbjct 79 ESMELIKRYRDINDRRVVIVELAEKG 104

>ref|NP_266269.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
 gb|AAK04211.1|AE006249_8 **G** transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
 Length=163

GENE ID: 1113719 rnaD | transcription regulator
 [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41 HILMLLAEQISTNAKIAEKLKISPAAVTKALKKQEQELIKSSRATNDERVVLSLTEKA 100
 HIL L ++ T ++A KL ++ VT+A++ L + + + + ++ +D++ + + LT K
 Sbjct 53 HILSALTKEIDLIGIELATKLSVTRGGVTRAVQNLIKQFLTTYQSESDKKKIFYHLTVKG 112
 Query 101 VPAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
 VA H H+ ++ +K+ ++E+ +I FLS
 Sbjct 113 RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIILSFLS 150

>ref|YP_002352539.1| **G** transcriptional regulator, MarR family [Dictyoglomus turgidum
 DSM 6724]

gb|ACK41925.1| **G** transcriptional regulator, MarR family [Dictyoglomus turgidum
 DSM 6724]
 Length=145

GENE ID: 7081680 Dtur_0640 | transcriptional regulator, MarR family
 [Dictyoglomus turgidum DSM 6724]

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 33/118 (27%), Positives = 63/118 (53%), Gaps = 8/118 (6%)

Query 31 SDVKLTSTQEHILMLLAEQIS-TNAKIAEKLKISPAAVTKALKKQEQELIKSSRATNDE 89
 S +KL Q IL+LL+E+ T +I E +KI P+ V ++++++ L+ + R D+ .
 Sbjct 26 SGLKLYRGQAPILLLLSELDGLTQKEIVENMKIKPSTVAIMIRRMKKRGLVITKRDEKDK 85
 Query 90 RVVLSLTEKAVPVAKEHATHHEKTLSTYQEE--LGKFTDEEQEVISKFLSALTEEFQ 145
 R LT++ ++ +KT +E GN FT+EE+E + +L + + +
 Sbjct 86 RFSKVYLTD-----GRKFICKLKTKYQLEEECFGN-FTEERETLKNYLERIRDNL 138

>ref|ZP_01854255.1| probable marR-family transcription regulator [Planctomyces maris
 DSM 8797]

gb|EDL59963.1| probable marR-family transcription regulator [Planctomyces maris
 DSM 8797]
 Length=159

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/83 (34%), Positives = 46/83 (55%), Gaps = 2/83 (2%)

Query 26 LGKCESDVKLTSTQEHILMLLA--EQISTNAKIAEKLKISPAAVTKALKKQEQELIKSS 83
 G+ + LT +Q ++L +L + + +IA ++ A+T L +LQ QELIK +
 Sbjct 38 FGRLFREYGLTPSQYNVLRILRGERKPMPSLEIANRMIQVVPATGLLDRLQAQELIKRN 97
 Query 84 RATNDERVVLSLTEKAVPVAKE 106
 R T D RVV +T KA+ + KE
 Sbjct 98 RCTEDRRVVYIEITAKALKLLKE 120

>ref|YP_773280.1| **G** MarR family transcriptional regulator [Burkholderia ambifaria
 AMMD]

gb|ABI86946.1| **G** transcriptional regulator, MarR family [Burkholderia ambifaria
 AMMD]
 Length=164

GENE ID: 4309612 Bamb_1388 | MarR family transcriptional regulator
 [Burkholderia ambifaria AMMD]

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKQEQELIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEEIGITGTQASMLFMIAVGRCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI 99
 Query 87 NDERVVLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVRLLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMRLRRILSNY 154

>ref|ZP_01131766.1| transcriptional regulator, MarR family protein [Pseudoalteromonas
 tunicata D2]

gb|EAR30132.1| transcriptional regulator, MarR family protein [Pseudoalteromonas
 tunicata D2]
 Length=163

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/83 (34%), Positives = 47/83 (56%), Gaps = 1/83 (1%)

Query 28 KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKQEQELIKSSRAT 86

Sbjct 24 K + LTS Q +L +++Q . K IAE++ +S A +T L +L+ +EL+ R+T
 KLSKETGLTSPQLLVQAISQQDGMVMEIAEQINLSSATITSILDRLEIRELVIRERST 83

Query 87 NDERVVLWSLTKAVPVAKEHAT 109
 D+R V SLT+K + K+ T

Sbjct 84 TDKRRVGISLTDKGFDIKDSPT 106

>ref|ZP_00238819.1| transcriptional regulator, MarR family [Bacillus cereus G9241]
 gb|EAL13614.1| transcriptional regulator, MarR family [Bacillus cereus G9241]
 Length=152

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

Query 35 LTSTQEHILMLLAEQISTNA-KIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVL 93
 LT Q +IL +L ++ A K+A+K+ + P+A+T + +L +QEL++ +D RVV+

Sbjct 35 LTPPQFYILKKILDHYGASRATKLAKKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVI 94

Query 94 WSLTEKAVPVAKEHATHHEKTLSTY 118
 LT+K +E T + ++ Y

Sbjct 95 IELTKKGKARVEEAMTARNEHIKY 119

>ref|YP_002467440.1| G transcriptional regulator, MarR family [Candidatus Methanosphaerula palustris El-9c]
 gb|ACL17717.1| G transcriptional regulator, MarR family [Candidatus Methanosphaerula palustris El-9c]
 Length=159

GENE ID: 7271351 Mpal_2438 | transcriptional regulator, MarR family
 [Candidatus Methanosphaerula palustris El-9c]

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 25/85 (29%), Positives = 47/85 (55%), Gaps = 0/85 (0%)

Query 56 IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTKAVPVAKEHATHHEKTL 115
 IA+ L ++P+A ++A+ KL + L+K R +ER V LT++ + H H++

Sbjct 53 IADLLGVTPSAASQAVTKLAGRGLVKKVRGKNEREVSLQDQGWVAYRYHEQTHKEIY 112

Query 116 STYQELGNKFTDEEQEVISKFLSAL 140
 + E ++EE E+I++F +A

Sbjct 113 TRTTERVGPLSEEELELIARFFNAF 137

>ref|ZP_03547491.1| hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
 gb|EED50137.1| hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
 Length=168

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/105 (30%), Positives = 53/105 (50%), Gaps = 4/105 (3%)

Query 41 HILMLLAEQISTN-AKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTK 99
 HI+ + E+ + N + +A+ L ++ +T A+ L ++ + R+ D RVVL SLT K

Sbjct 60 HIMEATGEENAKNMSSVAKLLSVTVGTLTIAINGLVKKGYVARERSEEDRRVVLISLTGK 119

Query 100 AVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 + H H+ + Q L DE+QE++ K L L E F

Sbjct 120 GRKANEEHKKFHDGMI---QALLKDLDDQEQEILVKSLNLREFF 161

>ref|ZP_02891041.1| transcriptional regulator, MarR family [Burkholderia ambifaria IOP40-10]
 gb|EDT03378.1| transcriptional regulator, MarR family [Burkholderia ambifaria IOP40-10]
 Length=163

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+

Sbjct 40 RTQEEELGITGTQASMLFMIAGVKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI 99

Query 87 NDERVVLWSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +

Sbjct 100 EDRRVVRLLELTDEGRELAERLPPVFRSVL---DELLGGFTPEEVGFLKSMRLRRILSNY 154

>ref|YP_001808132.1| G MarR family transcriptional regulator [Burkholderia ambifaria MC40-6]
 gb|ACB63916.1| G transcriptional regulator, MarR family [Burkholderia ambifaria MC40-6]
 Length=164

GENE ID: 6177160 BamMC406_1428 | MarR family transcriptional regulator
 [Burkholderia ambifaria MC40-6]

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+

Sbjct 40 RTQEEELGITGTQASMLFMIAGVKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI 99

Query 87 NDERVVLWSLTKAVPVAKETHHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVVRLTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMRLRRILSNY 154

>ref|ZP_02906301.1| transcriptional regulator, MarR family [Burkholderia ambifaria MEX-5]
 gb|EDT42559.1| transcriptional regulator, MarR family [Burkholderia ambifaria MEX-5]
 Length=164

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT 86
 + + ++ +T QO +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEELGITGTQASMLFMIAVGKCSAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI 99

Query 87 NDERVVLWSLTKAVPVAKETHHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVVRLTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMRLRRILSNY 154

>ref|ZP_02362996.1| transcriptional regulator, MarR family protein [Burkholderia oklahomensis C6786]
 Length=165

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVKLSTQEHILMLLA-EQISTNAKIAEKLKIS 63
 QI+ +G +M ++ ++ +++++ +T QO +L +LA + ST A++A + I R+
 Sbjct 17 QINDSVGYLMSRVKSLMTNMVQTQTQELGITGTQATMLFMLAVGKCSAAELAREYGID 76

Query 64 PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTKAVPVAKETHHHEKTLSTYQELGN 123
 +A+T+ L +++++ L++ R++ D RVV LT++ + + L ++ +
 Sbjct 77 ASAITRLDRVEKRGLLQVRSSDDRVRVRLTDEGRDLTRMPAIFRSVL---DQVLD 133

Query 124 KFTDEE 129
 FT EE
 Sbjct 134 GFTPEE 139

>ref|NP_977055.1| **G** MarR family transcriptional regulator [Bacillus cereus ATCC 10987]
 gb|AAS39663.1| **G** transcriptional regulator, MarR family [Bacillus cereus ATCC 10987]
 Length=152

GENE ID: 2747926 BCE_0730 | MarR family transcriptional regulator
 [Bacillus cereus ATCC 10987] (10 or fewer PubMed links)

Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

Query 35 LTSTQEHILMLLAEQISTNA-KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL 93
 LT Q +IL +L ++ A K+A+K+ + P+A+T + +L +QEL++ +D RVV+
 Sbjct 35 LTPPQFYILKILDHYGASRATKLAKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVV 94

Query 94 WSLTKAVPVAKETHHHEKTLSTY 118
 LT+K +E T + ++ Y
 Sbjct 95 IELTKKGKARVEEAMTARNEHI AKY 119

>ref|NP_782475.1| **G** MarR family transcriptional regulator [Clostridium tetani E88]
 gb|AAO36412.1| **G** transcriptional regulator, marR family [Clostridium tetani E88]
 Length=154

GENE ID: 1058804 marR | MarR family transcriptional regulator
 [Clostridium tetani E88] (10 or fewer PubMed links)

Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 25/91 (27%), Positives = 50/91 (54%), Gaps = 0/91 (0%)

Query 51 STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTKAVPVAKETHH 110
 + +IA L I+ +AV+K +++LQ++ LI SS+ +++ + ++LT + + K+H
 Sbjct 50 ANGTQIANYLNITRSVSKIIIRRLQENLISSQKPDNKKEIFYTLTNEGNNIFKQHKQA 109


Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
 HEK + + E+E + KFL
 Sbjct 110 HEKWEIRDTKFLKTISTNEKETVFKFLKKN 140


>ref|ZP_03570809.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2M]
 ref|ZP_03577696.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2]
 ref|ZP_03586132.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD1]
 gb|EED99839.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD1]
 gb|EEE07966.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2]
 gb|EEE14096.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2M]
 Length=164

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 32/118 (27%), Positives = 60/118 (50%), Gaps = 4/118 (3%)

```
Query 28 KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRAT 86
      ++ ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
Sbjct 40 RTQEELGITGTQASMLFMIAVGKCASTAAELAREYADASAVTRLDDRVEKRGLLCRVRSV 99

Query 87 NDERVVLWSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
      D RVV LT++ +A+ L Q LG FT EE + L + +
Sbjct 100 EDRRVVRELTDEGRALAERLPAIFRSVLD--QLLGG-FTPEEVGFLKSMRLRRILSNY 154
```

>ref|YP_001119315.1|  MarR family transcriptional regulator [Burkholderia vietnamiensis G4]

gb|ABO54480.1|  transcriptional regulator, MarR family [Burkholderia vietnamiensis G4]
Length=163


GENE ID: 4953186 Bcep1808_1472 | MarR family transcriptional regulator
[Burkholderia vietnamiensis G4]


Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 35/126 (27%), Positives = 66/126 (52%), Gaps = 5/126 (3%)

```
Query 6 QIDQFLGTIMQFAENKHEILLG-KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS 63
      QI+ +G +M ++ L+ + + ++ +T TQ +L ++A + ST A++A + I
Sbjct 17 QINDSGVGLMSRVKSVMTNLVTQRTQEELGITGTQASMLFMIAVGKCASTAAELAREYGID 76

Query 64 PAAVTKALKKLQEQLIKSSRATNDERVVLWSLTKAVPVAKEHATHHEKTLSTYQELGN 123
      +AVT+ L +++++ L+ R+ D RVV LT++ +A+ L EL
Sbjct 77 ASAVTRLDDRVEKRGLLSRVRSIEDRRVVRLELTDEGRALAERLPPVFRSVL---DELLE 133

Query 124 KFTDEE 129
      FT EE
Sbjct 134 GFTPEE 139
```

>ref|YP_002418276.1|  Histone acetyltransferase HPA2 and related acetyltransferases
[Vibrio splendidus LGP32]

emb|CAV19992.1|  Histone acetyltransferase HPA2 and related acetyltransferases
[Vibrio splendidus LGP32]
Length=301

GENE ID: 7162224 VS 2735 | Histone acetyltransferase HPA2 and related
acetyltransferases [Vibrio splendidus LGP32]

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 35/117 (29%), Positives = 60/117 (51%), Gaps = 1/117 (0%)

```
Query 25 LLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSR 84
      +L K +D+ L Q H L+ L +Q T ++A+KL I + ++A+ L+ LI++S
Sbjct 19 MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP 78

Query 85 ATNDERVVLWSLTKA-VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
      ND+R V+ S+T++ +AK H ++ S + L T + I +L AL
Sbjct 79 HPNDKRSVVASVTDQGKNTLAKLHNQQQFYDSVLEHLTEAETQQVSGGIEHYLKAL 135
```


>ref|ZP_02355848.1| transcriptional regulator, MarR family protein [Burkholderia
oklahomensis E0147]
Length=165

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

```
Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS 63
      QI+ +G +M ++ ++ +++++ +T TQ +L +LA + ST A++A + I
Sbjct 17 QINDSGVGLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCASTAAELAREYGID 76


Query 64 PAAVTKALKKLQEQLIKSSRATNDERVVLWSLTKAVPVAKEHATHHEKTLSTYQELGN 123
      +A+T+ L +++++ L++ R++ D RVV LT++ + + L ++ +
Sbjct 77 ASAITRLDDRVEKRGLLQVRVRSSEDRRVVRLELTDEGRELTRMPAIFRSVL---DQVLD 133

Query 124 KFTDEE 129
      FT EE
Sbjct 134 GFTPEE 139
```

>ref|YP_443075.1|  MarR family transcriptional regulator [Burkholderia thailandensis
E264]

ref|ZP_02374954.1| transcriptional regulator, MarR family protein [Burkholderia
thailandensis TXDOH]

ref|ZP_02388872.1| transcriptional regulator, MarR family protein [Burkholderia
thailandensis Bt4]

gb|ABC39239.1|  transcriptional regulator, MarR family [Burkholderia thailandensis
E264]
Length=165

GENE ID: 3849294 BTH_I2558 | MarR family transcriptional regulator
[Burkholderia thailandensis E264] (10 or fewer PubMed links)

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 33/126 (26%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

```

Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS 63
Sbjct 17 QI+ +G +M ++ ++ + +++++ +T TQ +L +LA + ST A++A + I 76
QINDSVGYLMSRVKSLMTNMVTQRTQTTELGITGTQATMLFMLAVGKCSTAAELAREYGID

Query 64 PAAVTKALKKKLQEQELIKSSSRATNDERVVLSLTKAVPVAKEHATHHEKTLSTYQELGN 123
Sbjct 77 +A+T+ L +++++ L++ R++ D RVV LT++ + K L E 123
ASAITRLLDRVEKRGLLQVRSSSEDRRVVRLLELTDEGRELTKRMPFIFRSVLDQVLE--- 133

Query 124 KFTDEE 129
FT EE
Sbjct 134 GFTPEE 139

```

```

>ref|ZP_02633998.1| transcriptional regulator, MarR family [Clostridium perfringens
E str. JGS1987]
ref|ZP_02636384.1| transcriptional regulator, MarR family [Clostridium perfringens
B str. ATCC 3626]
ref|ZP_02643088.1| transcriptional regulator, MarR family [Clostridium perfringens
NCTC 8239]
7 more sequence titles

```

```

ref|ZP_02629009.2| transcriptional regulator, MarR family [Clostridium perfringens
C str. JGS1495]
ref|ZP_02954000.1| transcriptional regulator, MarR family [Clostridium perfringens
D str. JGS1721]
gb|EDS81585.1| transcriptional regulator, MarR family [Clostridium perfringens
C str. JGS1495]
gb|EDT13394.1| transcriptional regulator, MarR family [Clostridium perfringens
E str. JGS1987]
gb|EDT23419.1| transcriptional regulator, MarR family [Clostridium perfringens
B str. ATCC 3626]
gb|EDT71039.1| transcriptional regulator, MarR family [Clostridium perfringens
D str. JGS1721]
gb|EDT77904.1| transcriptional regulator, MarR family [Clostridium perfringens
NCTC 8239]
Length=154

```

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 33/99 (33%), Positives = 50/99 (50%), Gaps = 5/99 (5%)

```

Query 48 EQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSSRATNDERVVLSLTKAVPVAKEH 107
E+ T +++A LKI+ +T A+ KL ++ + R D RVV+ LTK K H
Sbjct 49 EKARTMSEVALDLKITVGTLTAINKLIKGYVNRRIEEDRRVVMIELTEKGTLAYKVH 108

Query 108 ATHHEKTLSTYQELGNKFTDEEQEISKFLSALTEEFQ 145
HE+ + +ELG E+EV+ L L + FQ
Sbjct 109 EKFHEEMIDHVLEELGVS----EEVLISLSDKLDKFFQ 143

```

```

>ref|YP_001374721.1| G MarR family transcriptional regulator [Bacillus cereus subsp.
cytotoxIs NVH 391-98]
gb|ABS21726.1| G transcriptional regulator, MarR family [Bacillus cereus subsp.
cytotoxis NVH 391-98]
Length=136

```

GENE ID: 5344927 Bcer98_1405 | MarR family transcriptional regulator
[Bacillus cereus subsp. Cytotoxis NVH 391-98]

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 37/119 (31%), Positives = 62/119 (52%), Gaps = 4/119 (3%)

```

Query 28 KCESDVKLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKKLQEQELIKSSSRAT 86
+CE + L+ IL + + + T +KIA +L +S ++ +K+L +++LI R
Sbjct 16 RCEYENNLHQAIRILQITSREAETTISKIASELNLSHNTASEHVKRLIQDLILKERNK 75

Query 87 NDERVVLSLTKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEISKFLSALTEEFQ 145
DERVV +LT K +H EK L L ++ + EEQ++I + S L +E Q
Sbjct 76 KDERVVNLALTAKGKEALIKHTLLDEKKLKI---LESQLSKEEQIIEQAFSILAKEAQ 131

```

```

>ref|YP_819461.1| G transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides
ATCC 8293]
gb|ABJ63088.1| G Transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides
ATCC 8293]
Length=146

```

GENE ID: 4423731 LEUM_2018 | transcriptional regulator
[Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
(10 or fewer PubMed links)

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 30/84 (35%), Positives = 46/84 (54%), Gaps = 5/84 (5%)

```

Query 34 KLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSSRATNDERVV 92
K+ STQ H+LMLL Q TN ++A + +S A+TKA+K L + + +D+R
Sbjct 32 KINSTQAHLLMLLKILQSQTNTLAAAMNLSKPAITKAIKNLMRYHYVIAVVDDSDKRST 91

Query 93 LWSLTKAVPVA----KEHATHHE 112
+ LTE +A + HAT H+
Sbjct 92 HYLLTEDGEKLAQLHEQAHAHATMHD 115

```

```

>ref|ZP_02027443.1| hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC
27560]

```

gb|EDM50067.1| hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC 27560]
Length=151

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 27/90 (30%), Positives = 53/90 (58%), Gaps = 3/90 (3%)

```
Query 56 IAEKLIKSPAAVTKALKKLQEQELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTL 115
          IA+K+KI+ ++T ++ L ++ ++ +R+ D R+V +LTEK + K H HEK
Sbjct 60 IAKKMKITVGSLTSMNSLVKKHYVERNRRSEEDRRIVNITLTEKGIKAYKHHEEFHEK-- 117

Query 116 STYQELGNKFTDEEQEVISKFLSALTEEFQ 145
          Q ++ +++E +V+ K L+ L++ F
Sbjct 118 -MSQAAISEMSEDEVKVLKSLNNLSKFFH 146
```

Select All [Get selected sequences](#) [Distance tree of results](#)



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& BIOLOGIE MATHÉMATIQUE

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INGÉNIEUR ENSAIA

SANDRA MENA ②②
INGÉNIEUR ESCOM

DAVID GHIBAUDO ②
DOCTEUR EN MICROBIOLOGIE/VIROLOGIE

SERVICE JURIDIQUE

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GENEVIÈVE VU THANH ②②
LICENCIÉE EN DROIT DES AFFAIRES

FABRICE PIGEAUX ②②
DESS DROIT DU MSI

ELISABETH FOSSOT ②②
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DESS « ACCORDS ET PROPRIÉTÉ INDUSTRIELLE »

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THE NATH LAW GROUP
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ETATS-UNIS D'AMERIQUE

Attention : M. William E. BEAUMONT

Paris, March 5, 2009

UNITED STATES OF AMERICA - PATENT APPLICATION No. 10/525,449
filed on : August 29, 2003

In the name of: INSTITUT NATIONAL DE LA RECHERCHE
AGRONOMIQUE.

For : « Zinc-regulated prokaryotic expression cassettes. »

Invention : POQUET Isabelle, LLULL Daniel

Y/Ref.: 1169-034

O/Ref.: MJ/P/DG/md - F053900116/US/PCT

Dear Sir,

We refer to your letter of October 31, 2008 transmitting us the 1st Office Action
issued in relation with the above-referred application.

We have discussed this case with the applicant, and beg you to find herein enclosed
our comments and instructions concerning this application.

Since we believe that an interview with the Examiner will be necessary in order to
discuss the objections and the possible amendments to the claims, you may request a
third month extension of time.

Please acknowledge receipt of this letter by return.

In the meantime, we are,

Very truly yours,

M.J. VIALLE-PRESLES

B. ORES

Encl. : - Memorandum, and
- Annexes (only by e-mail).

U.S Application 10/1525449

**MEMORANDUM OF INSTRUCTIONS FOR RESPONDING THE OFFICE
ACTION OF OCTOBER 7, 2008**

1) Claims objections:

We beg you to amend the claims as requested by the Examiner. Concerning claim 15, it differs from claim 12 in that the expression cassette does not comprise the sequence encoding the ZitR repressor (cf § [0025] to [0027] of the instant application), and can be used to obtain constitutive expression of a protein of interest in bacterial strains wherein the endogenous ZitR repressor is inactivated (cf. § [0053] of the instant application)

2) Rejection under 35 USC § 112.

We wish to point out that the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

The results of BLAST searches using GENBANK AAK06214 as a query are enclosed therein. A first search was performed against all the protein sequences available in the nr database (all known protein sequences, including the complete sequences of various bacteria). The enclosed results (Annex 1) show that the only proteins having more than 80% identity with GENBANK AAK06214 (which is the ZitR protein of *Lactococcus lactis* subsp. *lactis* Il1403), are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).

A second search was performed against the whole genome sequences of *Lactococcus lactis* subsp. *lactis* Il1403, *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363. The enclosed results (Annex 2) show that the only lactococcal proteins having more than 80% identity with GENBANK AAK06214, are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).

Therefore, obtaining a nucleotide sequence encoding a protein having more than 80% identity with GENBANK AAK06214 would not have required require undue experimentation for one of skill in the art. He would have easily obtained it by routine screening of a lactococcal DNA library with a probe derived from the nucleotide sequence encoding GENBANK AAK06214 (or from nucleotides 357-794 of SEQ ID NO:2), and would inevitably have found the orthologs of GENBANK AAK06214.

We beg you to request an interview with the Examiner in order to discuss this issue of enablement. If necessary, you may amend paragraph b) of claim 12 so as to

specify that the polypeptide is a lactococcal polypeptide, and/or to indicate a higher percent of identity (85% rather than 80%) with GENBANK AAK06214.

3) Rejection under 35 USC § 102.

We beg you to insert in claims 12 and 15 the same disclaimer as in claim 18, which excludes the cassette and vector of POQUET et al.

BLAST Basic Local Alignment Search Tool

[Formatting options](#) [Download](#)

gb|AAK06214| (145 letters)

Results for: [gb|AAK06214.1 zinc transport transcriptional regulator \[Lactococcus lactis subsp. lactis II1403\]\(145aa\)](#)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|12725171|gb|AAK06214.1|AE006439_11

Description

zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403]

Molecule type

amino acid

Query Length

145

Database Name

3 databases

Description

Program

BLASTP 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,055,736
Number of sequences	7,259
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041

Results Statistics

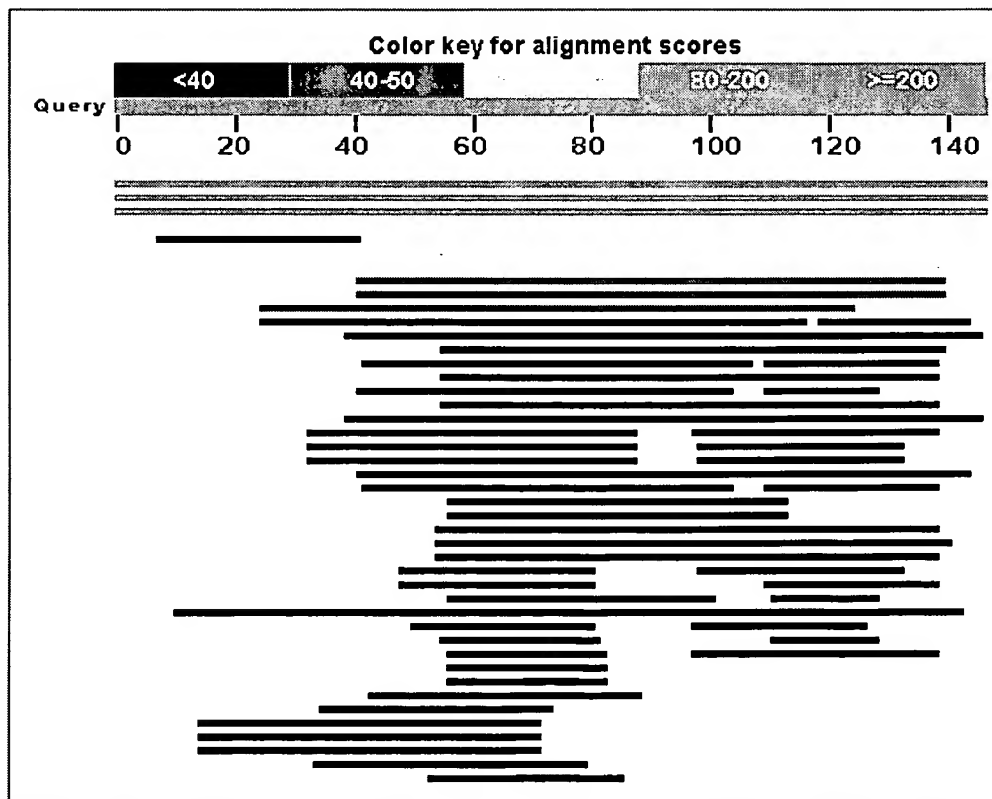
Length adjustment 78.
Effective length of query 67
Effective length of database 1489534
Effective search space 99798778
Effective search space used 99798778

Graphic Summary

Distribution of 58 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Sequences producing significant alignments:		Score (Bits)	E Value	
ref NP_268273.1	zinc transport transcription regulator [Lact...	291	2e-80	G
ref YP_811979.1	transcriptional regulator [Lactococcus lacti...	268	2e-73	G
ref YP_001033643.1	transcriptional regulator of the zit oper...	267	3e-73	G
ref YP_001033131.1	MarR family transcriptional regulator [La...	33.9	6e-09	G
ref YP_808726.1	transcriptional regulator [Lactococcus lacti...	51.2	4e-08	G
ref NP_266864.1	transcription regulator [Lactococcus lactis ...	51.2	4e-08	G
ref YP_808147.1	transcriptional regulator [Lactococcus lacti...	50.4	7e-08	G
ref YP_001031482.1	MarR family transcriptional regulator [La...	49.3	1e-07	G
ref NP_266269.1	transcription regulator [Lactococcus lactis ...	46.2	1e-06	G
ref NP_267626.1	transcription regulator [Lactococcus lactis ...	41.2	4e-05	G
ref YP_001032345.1	MarR family transcriptional regulator [La...	38.9	2e-04	G
ref YP_808779.1	transcriptional regulator [Lactococcus lacti...	37.0	9e-04	G
ref NP_266463.1	MarR family transcriptional regulator [Lacto...	36.2	0.001	G
ref NP_266747.1	transcription regulator [Lactococcus lactis ...	35.8	0.002	G
ref YP_001031675.1	MarR family transcriptional regulator [La...	35.4	0.002	G
ref NP_266396.1	MarR family transcriptional regulator [Lacto...	35.4	0.002	G
ref YP_808372.1	MarR family transcriptional regulator [Lacto...	35.4	0.002	G
ref YP_001031774.1	transcriptional regulator [Lactococcus la...	35.0	0.003	G
ref YP_001031679.1	putative transcriptional regulator [Lacto...	32.3	0.017	G
ref YP_808573.1	BadM/Rrf2 family transcriptional regulator [...	32.3	0.018	G
ref NP_266714.1	hypothetical protein L153086 [Lactococcus la...	32.3	0.018	G
ref YP_001033090.1	MarR family transcriptional regulator [La...	31.6	0.031	G
ref YP_808765.1	MarR family transcriptional regulator [Lacto...	31.6	0.034	G
ref YP_808735.1	MarR family transcriptional regulator [Lacto...	31.2	0.044	G
ref NP_266926.1	MarR family transcriptional regulator [Lacto...	31.2	0.045	G
ref YP_001032909.1	MarR family transcriptional regulator [La...	28.9	0.18	G
ref YP_001032520.1	MarR family transcriptional regulator [La...	28.1	0.31	G
ref NP_267064.1	transcription regulator [Lactococcus lactis ...	28.1	0.35	G
ref YP_001032533.1	transcriptional regulator [Lactococcus la...	28.1	0.38	G
ref YP_808312.1	Mn-dependent transcriptional regulator [Lact...	28.1	0.38	G
ref NP_267461.1	transcription regulator [Lactococcus lactis ...	27.7	0.42	G
ref NP_267696.1	transcription regulator [Lactococcus lactis ...	27.3	0.61	G
ref NP_266753.1	NADPH-flavin oxidoreductase [Lactococcus lac...	27.3	0.67	G
ref NP_267412.1	metalloregulator [Lactococcus lactis subsp. ...	26.6	1.1	G
ref YP_001031697.1	putative cobalt ABC transporter ATP-bindi...	26.2	1.2	G
ref NP_266573.1	quinone oxidoreductase [Lactococcus lactis s...	25.4	2.4	G
ref NP_268402.1	alkylphosphonate uptake protein [Lactococcus...	25.4	2.4	G
ref YP_808209.1	transcriptional repressor CodY [Lactococcus ...	24.6	3.4	G
ref YP_001031533.1	transcriptional repressor CodY [Lactococc...	24.6	3.4	G
ref NP_266317.1	transcriptional repressor CodY [Lactococcus ...	24.6	3.5	G
ref NP_266638.1	intercellular adhesion protein [Lactococcus ...	24.6	3.6	G
ref NP_266710.1	transcription regulator [Lactococcus lactis ...	24.6	3.6	G
ref NP_266438.1	amino acid amidohydrolase [Lactococcus lacti...	24.6	4.1	G
ref YP_808446.1	lysyl-tRNA synthetase [Lactococcus lactis su...	24.6	4.3	G
ref YP_001031741.1	lysyl-tRNA synthetase [Lactococcus lactis...	24.3	4.7	G
ref NP_266529.1	lysyl-tRNA synthetase [Lactococcus lactis su...	24.3	4.7	G
ref YP_001031907.1	NADPH-flavin oxidoreductase [Lactococcus ...	24.3	5.2	G
ref YP_808603.1	NADPH-flavin oxidoreductase [Lactococcus lac...	24.3	5.5	G
ref NP_268293.1	exported serine protease [Lactococcus lactis...	23.9	6.1	G
ref YP_001033660.1	housekeeping protease [Lactococcus lactis...	23.9	6.5	G
ref YP_811825.1	trypsin-like serine protease [Lactococcus la...	23.9	6.6	G
ref NP_268332.1	hypothetical protein L35545 [Lactococcus lac...	23.5	7.5	G

ref NP_268337.1 	hypothetical protein L39650 [Lactococcus lac...	23.5	7.7	
ref YP_001032772.1 	superfamily II DNA/RNA helicase [Lactococ...	23.5	7.8	
ref YP_001033122.1 	quinone oxidoreductase [Lactococcus lacti...	23.5	9.3	
ref YP_268733.1 	quinone oxidoreductase [Lactococcus lactis s...	23.5	9.3	
ref YP_795521.1 	hypothetical protein LACR_C57 [Lactococcus l...	23.5	9.5	
ref YP_211095.1 	hypothetical protein LACR_2554 [Lactococcus ...	23.1	10.0	

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>[ref|NP_268273.1|](#) zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=145

GENE ID: 1115793 zitR | zinc transport transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 2e-80, Method: Compositional matrix adjust.
Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

```

Query 1      MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL
Sbjct 1      MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60

Query 61     KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE
Sbjct 61     KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120

Query 121    LGNKFTDEEQEVISKFLSALTEEFQ 145
            LGNKFTDEEQEVISKFLSALTEEFQ
Sbjct 121    LGNKFTDEEQEVISKFLSALTEEFQ 145

```

>[ref|YP_811979.1|](#) transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=145

GENE ID: 4433026 LACR 2420 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 268 bits (685), Expect = 2e-73, Method: Compositional matrix adjust.
Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```

Query 1      MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct 1      MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQ 60

Query 61     KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHA HHEKTLSTYQE
Sbjct 61     KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAAHHEKTLSTYQE 120

Query 121    LGNKFTDEEQEVISKFLSALTEEFQ 145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct 121    LGDKFTDEEQKVISQFLSVLTFEFR 145

```

>[ref|YP_001033643.1|](#) transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145

GENE ID: 4799067 zitR | transcriptional regulator of the zit operon
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 267 bits (682), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```

Query 1      MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct 1      MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQ 60

Query 61     KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKA+PVAKEHA HHEKTLSTYQE
Sbjct 61     KISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAIPVAKEHAAHHEKTLSTYQE 120

Query 121    LGNKFTDEEQEVISKFLSALTEEFQ 145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct 121    LGDKFTDEEQKVISQFLSVLTFEFR 145

```

>[ref|YP_001033131.1|](#) MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=295

GENE ID: 4797387 rmaB | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

```
Query 42  ILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQLIKSSSRATNDERVVLWSLTEKAV 101
          ++ L E TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTEK
Sbjct 47  LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR 106

Query 102 PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE 142
          + T H T GN TDEEQE ++ + L E
Sbjct 107 EAQETRDTMHNDISETI--FGN-LTDEEQEQLANLMEKLVE 144
```

>ref|YP_808725.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=292

GENE ID: 4432217 LACR 0742 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query 52  TNAKIAEKLKISPAAVTKALKKKLQEQLIKSSSRATNDERVVLWSLTEKAVPVAKEHATHH 111
          TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTEK + T H
Sbjct 57  TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTMH 116

Query 112 EKTLSYQELGNKFTDEEQEVISKFLSALTE 142
          T GN TDEEQ+ ++ + L E
Sbjct 117 NDISETI--FGN-LTDEEQQLANLMEKLVE 144
```

>ref|NP_266864.1| **G** transcription regulator [Lactococcus lactis subsp. lactis I11403]
Length=291

GENE ID: 1114333 rmaB | transcription regulator
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query 52  TNAKIAEKLKISPAAVTKALKKKLQEQLIKSSSRATNDERVVLWSLTEKAVPVAKEHATHH 111
          TNA+IAE L I P++VT +K+L+E E++ + ND+RV LT+K + T H
Sbjct 57  TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTMH 116

Query 112 EKTLSYQELGNKFTDEEQEVISKFLSALTE 142
          T GN TDEEQE ++ + L E
Sbjct 117 NDISETI--FGN-LTDEEQQLAFLMEKLVE 144
```

>ref|YP_808147.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=169

GENE ID: 4432499 LACR 0099 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 50.4 bits (119), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query 41  HILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQLIKSSSRATNDERVVLWSLTEKA 100
          HIL L ++ T ++A KL ++ VT+A++ L + + + +A ND++ + + +T K
Sbjct 53  HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG 112

Query 101 VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
          + VA H H+ ++ +K+ + E+ +I FLS
Sbjct 113 LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIILNFLS 150
```

>ref|YP_001031482.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query 41  HILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQLIKSSSRATNDERVVLWSLTEKA 100
          HIL L ++ T ++A KL ++ VT+A++ L + + + +A ND++ + + +T K
Sbjct 56  HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG 115

Query 101 VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
          + VA H H+ ++ +K+ + ++ +I FLS
Sbjct 116 LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIILNFLS 153
```

>ref|NP_266269.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=163

GENE ID: 1113719 *rmaD* | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 46.2 bits (108), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query 41  HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEELIKSSRATNDERVVLWSLTEKA 100
          HIL L ++ T ++A KL ++ VT+A++ L + + + + ++ +D++ + + LT K
Sbjct 53  HILSALTKEDLTGIELATKLSVTRGGVTRAVQNLIKYQFLTYYQSESDKKKIFYHLTVKG 112

Query 101 VPAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
          VA H H+ ++ +K+ ++E+ +I FLS
Sbjct 113 RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIILSFLS 150
```

>ref|NP_267628.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=356

GENE ID: 1115129 *rmaC* | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 41.2 bits (95), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 29/100 (29%), Positives = 52/100 (52%), Gaps = 1/100 (1%)

```
Query 25  LLGCESDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEELIKSS 83
          + K E + T+ ++M+L + + +++ +LKI AAVT+ LK L+E+ L+K
Sbjct 20  MTAKFEKSTGYSITRYQLMMILKCKGRCSQSQQLQNELKIDSAAVTRHLKLLEKNLVKRE 79

Query 84  RATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN 123
          R + R V +T+KA A H+ +L Q++ N
Sbjct 80  RNKENNREVFVEITDKAKNDLALCAKKHDDSLDESQIILN 119
```

>ref|YP_001032345.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MGL363]
Length=139

GENE ID: 4798214 *rmaC* | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MGL363] (10 or fewer PubMed links)

Score = 38.9 bits (89), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 25/92 (27%), Positives = 49/92 (53%), Gaps = 1/92 (1%)

```
Query 25  LLGCESDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEELIKSS 83
          + K E + T+ ++M+L + + ++ +LKI AAVT+ LK L+E+ L+K
Sbjct 20  MTAKFEKSTGFSITRYQLMMILKCKGRCSQTQLQNELKIDSAAVTRHLKLLEKNLVKRQ 79

Query 84  RATNDERVVLWSLTEKAVPVAKEHATHHEKTL 115
          R ++ R V +T++A + A H+ ++
Sbjct 80  RNKDNNREVFVEITDEAKADLERCAREHDNSV 111
```

>ref|YP_808479.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=166

GENE ID: 4433047 *LACR_0453* | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 37.0 bits (84), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 31/111 (27%), Positives = 54/111 (48%), Gaps = 13/111 (11%)

```
Query 39  QEHLMLLAEQISTNAKIAEK-----LKISPAAVTKALKKLQEELIKSSRATNDERVVL 93
          Q IL +L E N+K+ +K L + P + ++ +KKL++++ I + D+R +
Sbjct 43  QGQILNILME----NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI 98

Query 94  WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
          SLTEK V +E A E + FT+EE+ ++ + L E
Sbjct 99  ISLTEKGKAVLEESAEQTELVPG----IMTSFTEEEKIEFARLIGLQSEL 145
```

>ref|NP_266463.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=159

GENE ID: 1113917 *napB* | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 36.2 bits (82), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 23/84 (27%), Positives = 46/84 (54%), Gaps = 0/84 (0%)

```
Query 55  KIAEKLKISPAAVTKALKKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT 114
```

Annex 2

Sbjct 60 K+A L ++ A +K KKL ++ L++S + +++ + + LT++ + H + H+K
 KLAHHLYMTRGAASKIAKKLLKKNLVESYQIPQNKKEIYFRLTKEGQEINDRHESLHQKF 119

Query 115 LSTYQELGNKFTDEEQEVISKFLS 138
 Q + ++ TDE I KFL+

Sbjct 120 SEKDQVIFDELTDSESVNILEFLN 143

>ref|NP_266747.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
 Length=143

GENE ID: 1114211 rmaJ | transcription regulator
 [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 35.8 bits (81), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/65 (35%), Positives = 33/65 (50%), Gaps = 0/65 (0%)

Query 42 ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV 101
 I ML E T K+ E+L + ++ LK+L+ + I R+ DER V LT+K

Sbjct 40 IAMLAIENKMTINKLGEELSLDSGLSPLLKRLEAKGYIVRKRSDDKERSVELFLTDKGA 99

Query 102 PVAKE 106
 V KE

Sbjct 100 QVKKE 104

>ref|YP_001031675.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=157

GENE ID: 4798013 napB | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

Query 55 KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT 114
 K+A L ++ A +K KKL ++ LI+S + +++ + + LT++ + H + H+K

Sbjct 58 KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF 117

Query 115 LSTYQELGNKFTDEEQEVISKFL 137
 Q + ++ TDE I +FL

Sbjct 118 SQNDQVIFDELTDSEAVSNILEFL 140

>ref|NP_266898.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
 Length=158

GENE ID: 1114368 rmaA | MarR family transcriptional regulator
 [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 22/66 (33%), Positives = 36/66 (54%), Gaps = 3/66 (4%)

Query 41 HILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLT 97
 +L L++ I N +I + L I ++V +A+K L E+E + R D+RV SLT

Sbjct 42 QLCLISLYIKDNQSQEQTDDLSIDKSSVHRAIKGLIEKEYVSRVRDEKDKRVYRVSLT 101

Query 98 EKAQPV 103
 +KA +

Sbjct 102 QKARDI 107

>ref|YP_808372.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=157

GENE ID: 4434175 LACR_0343 | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

Query 55 KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT 114
 K+A L ++ A +K KKL ++ LI+S + +++ + + LT++ + H + H+K

Sbjct 58 KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF 117

Query 115 LSTYQELGNKFTDEEQEVISKFL 137
 Q + ++ TDE I +FL

Sbjct 118 SQNDQVIFDELTDSEAVSNILEFL 140

>ref|YP_001031774.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=166

GENE ID: 4798362 llmg_0424 | transcriptional regulator
[*Lactococcus lactis* subsp. *cremoris* MG1363] (10 or fewer PubMed links)

Score = 35.0 bits (79), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 29/111 (26%), Positives = 53/111 (47%), Gaps = 13/111 (11%)

```
Query 39 QEHILMLLAEQISTNAKIAEK-----LKISPAAVTKALKKLQEQLIKSSRATNDERVVL 93
          Q IL +L E N+K+ +K L + P + ++ +KKL++++ I + D+R +
Sbjct 43 QGQILNILME---NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI 98

Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
          SLTEK V +E + + FT+EE+ ++ + L E
Sbjct 99 ISLTEKGKAVLEESTEQTGRVPG-----IMTSFTEEEKIEFARLIGKLQSEL 145
```

>ref|YP_001031879.1| **G** putative transcriptional regulator [*Lactococcus lactis* subsp. *cremoris* MG1363]
Length=156

GENE ID: 4796958 llmg_0529 | putative transcriptional regulator
[*Lactococcus lactis* subsp. *cremoris* MG1363] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

```
Query 33 VKLTSTQE---HILMLLAE---QISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRA 85
          +KL+S E ++L++LA + ++ +A +LK+SP+ + K +K L ++ L++S+
Sbjct 1 MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKLVSPSYLKKIIKSLVDEGLLRSTTG 60

Query 86 TN 87
          N
Sbjct 61 KN 62
```

>ref|YP_808573.1| **G** BadM/Rrf2 family transcriptional regulator [*Lactococcus lactis* subsp. *cremoris* SK11]
Length=156

GENE ID: 4433945 LACR_0579 | BadM/Rrf2 family transcriptional regulator
[*Lactococcus lactis* subsp. *cremoris* SK11] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

```
Query 33 VKLTSTQE---HILMLLAE---QISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRA 85
          +KL+S E ++L++LA + ++ +A +LK+SP+ + K +K L ++ L++S+
Sbjct 1 MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKLVSPSYLKKIIKSLVDEGLLRSTTG 60

Query 86 TN 87
          N
Sbjct 61 KN 62
```

>ref|NP_266714.1| **G** hypothetical protein L153086 [*Lactococcus lactis* subsp. *lactis* I11403]
Length=156

GENE ID: 1114177 yffB | hypothetical protein
[*Lactococcus lactis* subsp. *lactis* I11403] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

```
Query 33 VKLTSTQE---HILMLLAE---QISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRA 85
          +KL+S E ++L++LA + ++ +A +LK+SP+ + K +K L ++ L++S+
Sbjct 1 MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKLVSPSYLKKIIKSLVDEGLLRSTPG 60

Query 86 TN 87
          N
Sbjct 61 KN 62
```

>ref|YP_001033090.1| **G** MarR family transcriptional regulator [*Lactococcus lactis* subsp. *cremoris* MG1363]
Length=160

GENE ID: 4798315 rmaA | MarR family transcriptional regulator
[*Lactococcus lactis* subsp. *cremoris* MG1363] (10 or fewer PubMed links)

Score = 31.6 bits (70), Expect = 0.031, Method: Compositional matrix adjust.
Identities = 29/107 (27%), Positives = 52/107 (48%), Gaps = 10/107 (9%)

```
Query 41 HILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLT 97
          +L L++ I N +I + L I ++V +A++ L E+E + R +D+R SLT
Sbjct 42 QLLCLISLYIKDNQSQEQTDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLT 101

Query 98 EKAVPVAK--EHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE 142
          +KA + E T + L L +E+E+ K L+ +T+
```

Sbjct 102 KKARAIQSQIEEMTKERENL-----LSEGIDPKEKEIAFKVLNQMTQ 143

>ref|YP_008765.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=155

GENE ID: 4432345 LACR 0786 | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 31.6 bits (70), Expect = 0.034, Method: Compositional matrix adjust.
Identities = 20/65 (30%), Positives = 36/65 (55%), Gaps = 3/65 (4%)

Query 42 ILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQLIKSSSRATNDERVVLWSLITE 98
+L L++ I N +I + L I ++V +A++ L E+E + R +D+R SLT+
Sbjct 43 LLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLTK 102
Query 99 KAVPV 103
KA +
Sbjct 103 KARAI 107

>ref|YP_008795.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]

ref|YP_001033061.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=146

GENE ID: 4433123 LACR 0820 | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 31.2 bits (69), Expect = 0.044, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

Query 56 IEAKLKISPAAVTKALKKLQEQLIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHE 112
IA+ K++ + +T L +L+++ I+ R+T D RV LT K + ATH E
Sbjct 57 IAKNQKLALSTITITILNRLEDKGYIERKRSTADRRVTHIILTSKGDEL---ATHRE 110

>ref|NP_266926.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis I11403]
Length=146

GENE ID: 1114397 rmaG | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 31.2 bits (69), Expect = 0.045, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

Query 56 IEAKLKISPAAVTKALKKLQEQLIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHE 112
IA+ K++ + +T L +L+++ I+ R+T D RV LT K + ATH E
Sbjct 57 IAKNQKLALSTITITILNRLEDKGYIERKRSTADRRVTHIILTSKGDEL---ATHRE 110

>ref|YP_001032909.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=154

GENE ID: 4797429 rmaH | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.9 bits (63), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 24/85 (28%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

Query 54 AKIAEKLKISPAAVTKALKKLQEQLIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
+KIA+ S A + L L+ + LI + D R +L ++T+K VA+E
Sbjct 51 SKIAKFTHTSTARIATILNNLESKNLITREISRTDRRKILVAITDKGRRVAEEIRVEACS 110
Query 114 TLS-TYQELGNKFTDEEQEVISKFL 137
L+ ++E+G + T+ E FL
Sbjct 111 NLARVFKEMGEERTESFIENFKMFL 135

>ref|YP_001032520.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=127

GENE ID: 4797914 rmaX | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.31, Method: Compositional matrix adjust.
Identities = 24/86 (27%), Positives = 36/86 (41%), Gaps = 6/86 (6%)

Query 54 AKIAEKLKISPAAVTKALKKLQEQLIKSSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
+ IA + S A V L L+E+ +I + D R +L LT+K KE T
Sbjct 29 SDIARYIGASTARVANILNNLEEKGMISREISREDRRKILVFLTDKGRKETKERRTR--- 85

Query 114 TLSTYQELGNKFTDEEQEVISKFLSA 139
 T + N F +E +F+ A
 Sbjct 86 ---TITRISNVFEAMGEERTQQFIEA 108

>ref|NP_267064.1| **G** transcription regulator [Lactococcus lactis subsp. lactis I11403]
 Length=T54

GENE ID: 1114538 **rmaH** | transcription regulator
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.35, Method: Compositional matrix adjust.
 Identities = 23/85 (27%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

Query 54 AKIAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
 +KIA+ S A + L L+ + L+ + D R +L ++T+K VA+E
 Sbjct 51 SKIAKFTHTSTARIATILNNLESKNLVTREISRTDRRKILVAITDKGRHVAEEIRVEACS 110
 Query 114 TLS-TYQELGNKFTDEEQEVISKFL 137
 L+ ++E+G + T+ E FL
 Sbjct 111 NLARVFEEMGEERTESFIENFKLFL 135

>ref|YP_001032533.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris
 MG1363]
 Length=217

GENE ID: 4798916 **llmg 1224** | transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
 Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

Query 48 EQISTNAKIAEKLKISPAAVTKALKKKLQEQELI 80
 E +S NA IA+KL +S + T+ +K+L ++EL+
 Sbjct 23 ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>ref|YP_809312.1| **G** Mn-dependent transcriptional regulator [Lactococcus lactis subsp.
 cremoris SK11]
 Length=217

GENE ID: 4432558 **LACR 1369** | Mn-dependent transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
 Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

Query 48 EQISTNAKIAEKLKISPAAVTKALKKKLQEQELI 80
 E +S NA IA+KL +S + T+ +K+L ++EL+
 Sbjct 23 ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>ref|NP_267461.1| **G** transcription regulator [Lactococcus lactis subsp. lactis I11403]
 Length=T56

GENE ID: 1114954 **rmaF** | transcription regulator
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 27.7 bits (60), Expect = 0.42, Method: Compositional matrix adjust.
 Identities = 15/45 (33%), Positives = 24/45 (53%), Gaps = 0/45 (0%)

Query 56 IAEKLKISPAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKA 100
 + E L IS A+ + L+E+EL+ ND+R+ LTE+
 Sbjct 63 LLEVLDISKQALNGPMNDLKEKELVHFKPNENDKRIKQLYLTEQG 107

>ref|NP_267696.1| **G** transcription regulator [Lactococcus lactis subsp. lactis I11403]
 Length=T48

GENE ID: 1115197 **rmaI** | transcription regulator
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 27.3 bits (59), Expect = 0.61, Method: Compositional matrix adjust.
 Identities = 32/142 (22%), Positives = 60/142 (42%), Gaps = 18/142 (12%)

Query 11 LGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-----IAEKLKIS 63
 +G +++ A N+ + + LT Q IL L Q ++ I + I
 Sbjct 8 IGRLLKVASNQMSREFDNFAAQDLTGQMSILDFLNQSEEDSGKEISQTMIELEFNIR 67
 Query 64 PAAVTKALKKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAT----HHEKTLSTYQ 119
 + T+ L++++++LIIK + D R LTE+ E T H++K L+
 Sbjct 68 RSTTTTEILQRMKRLIKRKASPTDARQKSVELTEEGKQYLPETIYIQGHNQKALAG-- 125
 Query 120 ELGNKFTDEEQEVISKFLSALT 141
 + EE + KFL+ +
 Sbjct 126 -----LSAEIEIAAVEKFLNNFS 142

>ref|NP_266753.1| **G** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. lactis I11403]
Length=216

GENE ID: 1114217 yfiJ | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)
Score = 27.3 bits (59), Expect = 0.67, Method: Compositional matrix adjust.
Identities = 11/29 (37%), Positives = 18/29 (62%), Gaps = 0/29 (0%)

Query 109 THHEKTLSTYQELGNKFTDEEQEVIKFL 137
+HH+K+ QE+ N T +E ++KFL
Sbjct 180 SHHQKSTDWTQEMSNFLTKPRREDVAKFL 208

>ref|NP_267412.1| **G** metalloregulator [Lactococcus lactis subsp. lactis I11403]
Length=217

GENE ID: 1114905 ymiA | metalloregulator
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)
Score = 26.6 bits (57), Expect = 1.1, Method: Compositional matrix adjust.
Identities = 13/31 (41%), Positives = 23/31 (74%), Gaps = 1/31 (3%)

Query 50 ISTNAKIAEKLKISPAAVTKALKKLQEQELI 80
+S NA IA+KL +S + T+ +K+L ++EL+
Sbjct 25 VSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>ref|YP_001031697.1| **G** putative cobalt ABC transporter ATP-binding protein [Lactococcus lactis subsp. cremoris MG1363]
Length=565

GENE ID: 4798558 cbiO | putative cobalt ABC transporter ATP-binding protein
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)
Score = 26.2 bits (56), Expect = 1.2, Method: Compositional matrix adjust.
Identities = 12/27 (44%), Positives = 17/27 (62%), Gaps = 0/27 (0%)

Query 55 KIAEKLKISPAAVTKALKKLQEQELIK 81
++A K ISP ++TKA Q QE +K
Sbjct 537 QLARKADISPISLTAKAFINFQNERLK 563

>ref|NP_266873.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. lactis I11403]
Length=328

GENE ID: 1114342 qor | quinone oxidoreductase
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)
Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 0/19 (0%)

Query 109 THHEKTLSTYQELGNKFTD 127
HHEK + ELG KF D
Sbjct 193 NHHEKLVQVHELGFKFVD 211

>ref|NP_268402.1| **G** alkylphosphonate uptake protein [Lactococcus lactis subsp. lactis I11403]
Length=114

GENE ID: 1115923 phnA | alkylphosphonate uptake protein
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)
Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
Identities = 14/41 (34%), Positives = 19/41 (46%), Gaps = 0/41 (0%)

Query 97 TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVIKFL 137
T K + + E+ T E GN+FT EE E KF+
Sbjct 3 TPKCIHCSSEYTYELSDTSFGCSECGNEFTLEEIEAAGKFI 43

>ref|YP_808209.1| **G** transcriptional repressor CodY [Lactococcus lactis subsp. cremoris SK11]
Length=262

GENE ID: 4434653 LACR 0168 | transcriptional repressor CodY
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)
Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56 IAEKLKISPAAVTKALKKLQEQELIKS 82
IA+K+ I+ + + AL+KL+ +I+S

Sbjct 210 IADKIGITRSVIVNALRKLESAGVIES 236

>ref|YP_001031533.1| **G** transcriptional repressor CodY [Lactococcus lactis subsp. cremori MG1363]
Length=262

GENE ID: 4797198 codY | transcriptional repressor CodY
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56 IAEKLIKISPAAVTKALKKKLQEQELIKS 82
IA+K+ I+ + + AL+KL+ +I+S
Sbjct 210 IADKIGITRSVIVNALRKLESAGVIES 236

>ref|NP_266317.1| **G** transcriptional repressor CodY [Lactococcus lactis subsp. lactis I11403]
Length=262

GENE ID: 1113769 codY | transcriptional repressor CodY
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.5, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56 IAEKLIKISPAAVTKALKKKLQEQELIKS 82
IA+K+ I+ + + AL+KL+ +I+S
Sbjct 210 IADKIGITRSVIVNALRKLESAGVIES 236

>ref|NP_266838.1| **G** intercellular adhesion protein [Lactococcus lactis subsp. lactis I11403]
Length=276

GENE ID: 1114306 icaB | intercellular adhesion protein
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 14/46 (30%), Positives = 21/46 (45%), Gaps = 0/46 (0%)

Query 43 IMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQELIKSSRATND 88
L L Q K+ + + S + K +KK+ E L+ S TND
Sbjct 126 LDLPFTQFIITGKVGQTIDGSQMSTWKEIKKMENPLVTSGLTND 171

>ref|NP_266710.1| **G** transcription regulator [Lactococcus lactis subsp. lactis I11403]
Length=247

GENE ID: 1114173 yfeA | transcription regulator
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 16/44 (36%), Positives = 25/44 (56%), Gaps = 5/44 (11%)

Query 35 LTSTQEHIMLLAEQIS-----TNAKIAEKLKISPAAVTKALKK 73
LTS + +I L E + T A+IAE +SP+++ + LKK
Sbjct 4 LTSVEIYIWNYLEENKAKIIQMTVAQIAESAHVSPSSIIRTLKK 47

>ref|NP_266438.1| **G** amino acid amidohydrolase [Lactococcus lactis subsp. lactis I11403]
Length=384

GENE ID: 1113892 yciA | amino acid amidohydrolase
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 4.1, Method: Compositional matrix adjust.
Identities = 11/41 (26%), Positives = 17/41 (41%), Gaps = 7/41 (17%)

Query 8 DQFLGT-----IMQFAENKHEILLGKCESDVKLTSTQEH 41
D+F G + A N+H + G CE ++ T H
Sbjct 147 DEFYGLHVRPDLKVGDIATNQHTLFAGTCEVELSFIGTGGH 187

>ref|YP_808446.1| **G** lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris SK11]
Length=494

GENE ID: 4433352 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 4.3, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98 EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
E+A +AKEH H EK ++ + N+F ++ E

Sbjct 340 EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>ref|YP_001031741.1| **G** lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris MG1363]
Length=494

GENE ID: 4799123 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98 EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
E+A +AKEH H EK ++ + N+F ++ E
Sbjct 340 EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>ref|NP_266529.1| **G** lysyl-tRNA synthetase [Lactococcus lactis subsp. lactis Il1403]
Length=494

GENE ID: 1113984 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98 EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
E+A +AKEH H EK ++ + N+F ++ E
Sbjct 340 EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>ref|YP_001031907.1| **G** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris MG1363]
Length=251

GENE ID: 4798593 l1mg_0559 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 5.2, Method: Compositional matrix adjust.
Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

Query 109 THHEKTLSTYQELGNKFTDEEQEVISKFL 137
+HH+K+ + QE+ + T+ +E ++ FL
Sbjct 215 SHHQKSTNWSQEMSDFLTNPREDLTDFL 243

>ref|YP_808603.1| **G** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=251

GENE ID: 4433732 LACR_0613 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 5.5, Method: Compositional matrix adjust.
Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

Query 109 THHEKTLSTYQELGNKFTDEEQEVISKFL 137
+HH+K+ + QE+ + T+ +E ++ FL
Sbjct 215 SHHQKSTNWSQEMSDFLTNPREDLADFL 243

>ref|NP_268293.1| **G** exported serine protease [Lactococcus lactis subsp. lactis Il1403]
Length=408

GENE ID: 1115813 htrA | exported serine protease
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.1, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15 MQFAENKHEI--LLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
+ FA +++ ++ K E+D K++ I M+ Q+STN + +LK+ P++VT +
Sbjct 271 LGFAIPSNVNIINKLEADGKISRPAIGIRMVDLSQLSTND--SSQLKL-PSSVTGGV 326

>ref|YP_001033660.1| **G** housekeeping protease [Lactococcus lactis subsp. cremoris MG1363]
Length=407

GENE ID: 4797497 htrA | housekeeping protease
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.5, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15 MQFAENKHEI--LLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
+ FA +++ ++ K E+D K++ I M+ Q+STN + +LK+ P++VT +
Sbjct 270 LGFAIPSNVNIINKLETGKISRPAIGIRMVDLSQLSTND--SSQLKL-PSSVTGGV 325

>ref|YP_811995.1| **G** trypsin-like serine protease [Lactococcus lactis subsp. cremoris SK11]
Length=407

GENE ID: 4432303 LACR_2439 | trypsin-like serine protease
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.6, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15 MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
+ FA +++ ++ K E+D K++ I M+ Q+STN + +LK+ P++VT +
Sbjct 270 LGFAIPSNDDVNIINKLETGDKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV 325

>ref|NP_268332.1| **G** hypothetical protein L35545 [Lactococcus lactis subsp. lactis I11403]

ref|YP_812032.1| **G** hypothetical protein LACR_2483 [Lactococcus lactis subsp. cremoris SK11]

ref|YP_001033699.1| **G** hypothetical protein llmg_2459 [Lactococcus lactis subsp. cremoris MG1363]
Length=82

GENE ID: 1115852 ywFB | hypothetical protein
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.5, Method: Compositional matrix adjust.
Identities = 13/29 (44%), Positives = 14/29 (48%), Gaps = 0/29 (0%)

Query 97 TEKAVPVAKEHATHHEKTLSTYQELGNKF 125
TE AKE A +E L YQ L KF
Sbjct 34 TEDGKKEAKEAAIRYESRLDAYQFLQGNKF 62

>ref|NP_268337.1| **G** hypothetical protein L39650 [Lactococcus lactis subsp. lactis I11403]
Length=926

GENE ID: 1115857 ywFG | hypothetical protein
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.7, Method: Composition-based stats.
Identities = 11/25 (44%), Positives = 13/25 (52%), Gaps = 0/25 (0%)

Query 118 YQELGNKFTDEEQEVISKFLSALTE 142
Y E G KF D+ Q I + LTE
Sbjct 557 YPEDGTRFADDPQHYIVRLKHGLTE 581

>ref|YP_001032772.1| **G** superfamily II DNA/RNA helicase [Lactococcus lactis subsp. cremoris MG1363]
Length=430

GENE ID: 4797767 comFA | superfamily II DNA/RNA helicase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.8, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 26/46 (56%), Gaps = 1/46 (2%)

Query 34 KLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKKLQEQEL 79
KLT QE I L +QI+ N K+ + ++ A T+ + +L EQ L
Sbjct 105 KLTENQEKISNALCQQITNNQKLLVQ-AVTGAGKTEMIYQLIEQIL 149

>ref|YP_001033122.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. cremoris MG1363]
Length=328

GENE ID: 4798878 qor | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)


Query 110 HHEKTLSTYQELGNKFTD 127
HHE + ELG KF D
Sbjct 194 HHENLVPQVHELGFKFVD 211

>ref|YP_808733.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=328

GENE ID: 4432226 LACR_0751 | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)


Query 110 HHEKTLSTYQELGNKFTD 127
HHE + ELG KF D
Sbjct 194 HHENLVPQVHELGFKEVD 211

>ref|YP_796521.1|  hypothetical protein LACR_C57 [Lactococcus lactis subsp. cremoris SK11]
Length=330

GENE ID: 4405852 LACR C57 | hypothetical protein
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.5, Method: Compositional matrix adjust.
Identities = 11/33 (33%), Positives = 22/33 (66%), Gaps = 0/33 (0%)

Query 53 NAKIAEKLKISPAAVTKALKKKLQEQELIKSSRA 85
N K ++L S + ++A K+Q Q+L+K+S++
Sbjct 189 NIKDTQELDFSSSNFSEAQLKVQNQDLVKNSKS 221

>ref|YP_812095.1|  hypothetical protein LACR_2554 [Lactococcus lactis subsp. cremoris SK11]
Length=114

GENE ID: 4432134 LACR 2554 | hypothetical protein
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.1 bits (48), Expect = 10.0, Method: Compositional matrix adjust.
Identities = 13/41 (31%), Positives = 18/41 (43%), Gaps = 0/41 (0%)

Query 97 TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL 137
T K + + E+ E GN+FT EE E KF+
Sbjct 3 TPKCIHCSSEYTYELSDMSFGCSECGNEFTLEEIEAAGKFI 43

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